

OM protein - protein search, using sw model

Run on: August 13, 2004, 09:06:38 ; Search time 4.74359 Seconds
 (without alignments)
 1250.845 Million cell updates/sec

Title: US-09-785-215-6
 Perfect score: 112
 Sequence: 1 FNNFTVSFWLRVPKVSASHLE 21

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	112	100.0	21	2	AAR11896	Aar11896 Immunogen
2	112	100.0	21	2	AAW06130	Aaw06130 Tetanus t
3	112	100.0	21	2	AAR88397	Aar88397 T-cell an
4	112	100.0	21	2	AAW46449	Aaw46449 Broad ran
5	112	100.0	21	2	AAW67034	Aaw67034 Tetanus t
6	112	100.0	21	2	AAW67579	Aaw67579 T-cell ep
7	112	100.0	21	2	AAW73222	Aaw73222 Tetanus t
8	112	100.0	21	3	AAY92626	Aay92626 Foreign e
9	112	100.0	21	3	AAY99876	Aay99876 Tetanus t

10	112	100.0	21	3	AAy84428	Aay84428	Amino aci
11	112	100.0	21	3	AAy49260	Aay49260	CD4+ T ce
12	112	100.0	21	3	AAB45512	Aab45512	Tetanus P
13	112	100.0	21	4	AAE11764	Aae11764	Clostridi
14	112	100.0	21	4	AAB49072	Aab49072	Tetanus t
15	112	100.0	21	4	AAB46173	Aab46173	Tetanus t
16	112	100.0	21	4	AAB68637	Aab68637	HER-2 B c
17	112	100.0	21	4	AAB61958	Aab61958	Tetanus T
18	112	100.0	21	4	AAB20144	Aab20144	Tetanus t
19	112	100.0	21	4	AAB85453	Aab85453	Universal
20	112	100.0	21	4	AAB85702	Aab85702	Amino aci
21	112	100.0	21	5	ABG31775	Abg31775	T helper
22	112	100.0	21	5	AAU11415	Aau11415	Tetanus t
23	112	100.0	21	6	ABP72695	Abp72695	Tetanus t
24	112	100.0	21	6	ADA25170	Ada25170	C. tetani
25	112	100.0	21	6	AAO30455	Aao30455	Tetanus t
26	112	100.0	21	7	ABR82483	Abr82483	Tetanus t
27	112	100.0	21	7	ADC09977	Adc09977	Tetanus t
28	112	100.0	21	7	ADC89659	Adc89659	C. tetani
29	112	100.0	21	7	ADC81610	Adc81610	Tetanus t
30	112	100.0	21	7	ADD71439	Add71439	HLA-DP4 b
31	112	100.0	28	4	AAB46176	Aab46176	Tetanus t
32	112	100.0	31	3	AAy92653	Aay92653	PSMpep010
33	112	100.0	31	3	AAy92654	Aay92654	PSMpep011
34	112	100.0	31	3	AAy92655	Aay92655	PSMpep012
35	112	100.0	32	2	AAR62702	Aar62702	LHRH-cont
36	112	100.0	33	4	AAB49075	Aab49075	Amyloid b
37	112	100.0	34	5	AAU11421	Aau11421	Synthetic
38	112	100.0	36	4	AAG63662	Aag63662	Peptide c
39	112	100.0	36	4	AAG63515	Aag63515	A peptide
40	112	100.0	37	5	AAU11425	Aau11425	Synthetic
41	112	100.0	43	4	AAB49076	Aab49076	Amyloid b
42	112	100.0	43	4	AAB46177	Aab46177	Tetanus t
43	112	100.0	44	4	AAB49090	Aab49090	Amyloid b
44	112	100.0	44	4	AAB46194	Aab46194	Tetanus t
45	112	100.0	50	5	AAU11429	Aau11429	Synthetic

ALIGNMENTS

RESULT 1

AAR11896

ID AAR11896 standard; peptide; 21 AA.

XX

AC AAR11896;

XX

DT 24-OCT-2003 (revised)

DT 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 19-JUL-1991 (first entry)

XX

DE Immunogenic conjugate constituent peptide, TT3.

XX

KW Malaria vaccine; major histocompatibility complex.

XX

OS Viruses.

XX
 FH Key Location/Qualifiers
 FT Peptide 1. .14
 FT /label= active fragment (claimed)
 XX
 PN EP427347-A.
 XX
 PD 15-MAY-1991.
 XX
 PF 07-NOV-1990; 90EP-00202948.
 XX
 PR 10-NOV-1989; 89IT-00022355.
 XX
 PA (ENIE) ENIRICERCHE SPA.
 XX
 PI Blanchi E, Pessi A, Corradin G;
 XX
 DR WPI; 1991-141874/20.
 XX
 PT Synthetic peptide(s) used as universal carriers - for preparing
 PT immunogenic conjugates used as vaccines against plasmodium falciparum.
 XX
 PS Claim 1; Page 13; 16pp; English.
 XX
 CC This peptide corresps. to residues 947-967 of Tetanus toxin. It can be
 CC used as a universal carrier for the prepn. of an immunogenic conjugate.
 CC It is covalently bound to a peptide or polysaccharide hapten derived from
 CC a pathogen. This conjugate can be used as a vaccine for malaria. This
 CC peptide is recognised by different T- helper cell clones in association
 CC with alleles of the human MHC. It contains 2 epitopes: (a) 953-967,
 CC recognised by DR5-restricted clones; and (b) 947-960, recognised by all
 CC other DR and DP- restricted clones. (Updated on 25-MAR-2003 to correct PI
 CC field.) (Updated on 27-AUG-2003 to correct OS field.) (Updated on 24-OCT-
 CC 2003 to standardise OS field)
 XX
 SQ Sequence 21 AA;

Query Match 100.0%; Score 112; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 6.3e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPKVSASHLE 21
 |||||
 Db 1 FNNFTVSFWLRVPKVSASHLE 21

RESULT 2

AAW06130

ID AAW06130 standard; peptide; 21 AA.

XX

AC AAW06130;

XX

DT 07-FEB-1997 (first entry)

XX

DE Tetanus toxoid protein T-cell epitope.

XX

KW Cholesteryl ester transfer protein; CETP; antigen; vaccine;

KW cardiovascular disease; atherosclerosis; tetanus toxoid; T-cell epitope.
 XX
 OS Clostridium tetani.
 XX
 PN WO9634888-A1.
 XX
 PD 07-NOV-1996.
 XX
 PF 01-MAY-1996; 96WO-US006147.
 XX
 PR 01-MAY-1995; 95US-00432483.
 XX
 PA (TCEL-) T CELL SCI INC.
 XX
 PI Rittershaus CW, Thomas LJ;
 XX
 DR WPI; 1996-506103/50.
 XX
 PT Cholesteryl ester transfer protein B cell epitope linked to T cell
 PT epitope - used to generate vaccine to regulate CETP activity for
 PT decreasing the risk of developing a cardiovascular disease e.g.
 PT atherosclerosis.
 XX
 PS Claim 11; Page 43; 72pp; English.
 XX
 CC A helper T-cell epitope (AAW06130) comprises amino acids 947-967 of
 CC tetanus toxoid protein. It can be utilised in novel peptide vaccines (see
 CC also AAW06129, AAW06132) also including B-cell epitope(s) from human or
 CC rabbit cholesteryl ester transfer protein (CETP) to elicit an immune
 CC response against endogenous CETP activity, thereby treating or preventing
 CC a cardiovascular disease, such as atherosclerosis
 XX
 SQ Sequence 21 AA;

Query Match 100.0%; Score 112; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 6.3e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSEFWLRVPKVSASHLE 21
 |||||
 Db 1 FNNFTVSEFWLRVPKVSASHLE 21

RESULT 3

AAR88397

ID AAR88397 standard; peptide; 21 AA.

XX

AC AAR88397;

XX

DT 12-JUN-1996 (first entry)

XX

DE T-cell antigen TT3 peptide.

XX

KW T-antigen; vaccine; antibody; T-cell; T-lymphocyte; alpha-helix;

KW coiled-coil heterodimer; core peptide; subunit.

XX

OS Synthetic.

XX
 PN WO9531480-A1.
 XX
 PD 23-NOV-1995.
 XX
 PF 18-MAY-1995; 95WO-CA000293.
 XX
 PR 18-MAY-1994; 94US-00245507.
 XX
 PA (SPIS-) SPI SYNTHETIC PEPTIDES INC.
 XX
 PI Houston ME, Zhou NE, Kay CM, Hodges RS, Cachia PJ, Irvin RT;
 XX
 DR WPI; 1996-010880/01.
 XX
 PT Hetero:dimeric polypeptide immunogen in coiled-coil configuration with
 PT different antigens on each sub:unit - useful in vaccines and for antibody
 PT prodn.
 XX
 PS Claim 7; Page 62; 95pp; English.
 XX
 CC This T-cell antigen TT3 peptide may be attached to a core peptide
 CC contained in one of the 2 subunits of an alpha-helical coiled-coil
 CC heterodimer. Each core peptide is comprised of terminal and internal AA
 CC repeat sequences. This peptide antigen is attached to the core peptide
 CC through covalent linkages to certain AA of the internal repeats. The 2
 CC subunits of the heterodimer are arranged in a stable alpha-helical coiled
 CC -coil configuration having a 1:1 stoichiometry, and the peptide antigen
 CC is disposed toward the outer surfaces of the configuration. The
 CC heterodimer may be used as a synthetic vaccine (optionally multivalent)
 CC or to generate antibodies
 XX
 SQ Sequence 21 AA;

Query Match 100.0%; Score 112; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 6.3e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPKVSASHLE 21
 |||||
 Db 1 FNNFTVSFWLRVPKVSASHLE 21

RESULT 4

AAW46449

ID AAW46449 standard; peptide; 21 AA.

XX

AC AAW46449;

XX

DT 18-MAY-1998 (first entry)

XX

DE Broad range helper T cell epitope from the tetanus toxoid protein.

XX

KW Cholesteryl ester transfer protein; CETP; cholesteryl ester;

KW high density lipoprotein; HDL; very low density lipoprotein; VLDL;

KW low density lipoprotein; LDL; T cell epitope; antibody;

KW DNA plasmid-based vaccine; broad range helper T cell epitope; treatment;

KW cardiovascular disease.
 XX
 OS Clostridium tetani.
 XX
 PN WO9741227-A1.
 XX
 PD 06-NOV-1997.
 XX
 PF 01-MAY-1997; 97WO-US007294.
 XX
 PR 01-MAY-1996; 96US-00640713.
 PR 21-FEB-1997; 97US-00802967.
 XX
 PA (TCEL-) T CELL SCI INC.
 XX
 PI Thomas LJ;
 XX
 DR WPI; 1997-549731/50.
 XX
 PT DNA plasmid-based vaccine encodes CETP B cell and helper T cell
 PT epitope(s) - used for elevating high density lipoprotein levels, and for
 PT treating cardiovascular disease.
 XX
 PS Disclosure; Page 44; 67pp; English.
 XX
 CC The present sequence represents a broad range helper T cell epitope of
 CC the tetanus protein. It can be used in DNA plasmid-based vaccines against
 CC cholesteryl ester transfer proteins (CETPs). CETPs mediate the transfer
 CC of cholesteryl esters from high density lipoprotein (HDL) to very low
 CC density lipoprotein (VLDL) and low density lipoprotein (LDL), and vice
 CC versa. An increased CETP activity produces an atherogenic lipoprotein
 CC profile and induces atherosclerosis. A DNA plasmid-based vaccine
 CC comprises sequences encoding at least one B cell epitope of CETP linked
 CC in frame with at least one segment encoding a broad range helper T cell
 CC epitope. The vaccines can be used to elevate the ratio of circulating HDL
 CC to circulating LDL, VLDL or total cholesterol in a human. It can also be
 CC used for decreasing the level of endogenous CETP activity in a human. The
 CC vaccine can be used to produce anti-CETP antibodies in vivo and for
 CC treating cardiovascular disease
 XX
 SQ Sequence 21 AA;

Query Match 100.0%; Score 112; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 6.3e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSEFWLRVPKVSASHLE 21
 |||||
 Db 1 FNNFTVSEFWLRVPKVSASHLE 21

RESULT 5
 AAW67034
 ID AAW67034 standard; peptide; 21 AA.
 XX
 AC AAW67034;
 XX

DT 15-DEC-1998 (first entry)
 XX
 DE Tetanus toxin fragment (residues 947-967).
 XX
 KW Tetanus toxin; vaccine; antibody; carbohydrate peptide conjugate;
 KW dendrimeric poly-lysine; epitope; tumour.
 XX
 OS Clostridium tetani.
 XX
 PN WO9843677-A1.
 XX
 PD 08-OCT-1998.
 XX
 PF 27-MAR-1998; 98WO-EP001922.
 XX
 PR 27-MAR-1997; 97US-0041726P.
 XX
 PA (INSP) INST PASTEUR.
 XX
 PI Bay S, Cantacuzene D, Leclerc C, Lo-Man R;
 XX
 DR WPI; 1998-557071/47.
 XX
 PT Carbohydrate peptide conjugate used as vaccine - comprises carrier with
 PT dendrimeric poly-lysine enabling multiple epitopes to be covalently
 PT attached.
 XX
 PS Disclosure; Page 13; 55pp; English.
 XX
 CC The invention relates to a new carbohydrate peptide conjugate, which
 CC comprises a carrier with a dendrimeric poly-lysine enabling multiple
 CC epitopes to be covalently attached to it. Also claimed are: (1) an
 CC antibody purified from biological fluid or cells of organisms
 CC administered with the carbohydrate peptide conjugate, and (2) a diagnosis
 CC kit comprising antigen-specific antibodies elicited by immunisation with
 CC the carbohydrate peptide conjugate. The peptide conjugate, antibody and
 CC diagnosis kit are used to provide pharmaceutical compositions and
 CC vaccines against tumours. These can be used to support an immune response
 CC against viral infections caused by hepatitis virus, HIV or cytomegalo
 CC virus. They can be used to enhance immune responses, especially B- and T-
 CC cell responses, of humans and animals against bacterial infections. The
 CC carbohydrate peptide conjugate stimulates the antibody and T-cell
 CC response without stimulating undesired immune responses. The composition
 CC is capable of increasing the survival of tumour bearing humans and
 CC animals. The present sequence corresponds to residues 947-967 of tetanus
 CC toxin. The synthetic peptide corresponding to this sequence may be used
 CC as an epitope in a carbohydrate peptide conjugate
 XX
 SQ Sequence 21 AA;

Query Match 100.0%; Score 112; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 6.3e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPKVSASHLE 21
 |||||
 Db 1 FNNFTVSFWLRVPKVSASHLE 21

RESULT 6

AAW67579

ID AAW67579 standard; peptide; 21 AA.

XX

AC AAW67579;

XX

DT 02-MAR-1999 (first entry)

XX

DE T-cell epitope peptide #5 for chimeric fimbrin/T-cell epitope peptide.

XX

KW Chimeric; non-typable Haemophilus influenzae; fimbrin; T-cell epitope;
KW immunogenic composition; immune response.

XX

OS Synthetic.

XX

PN US5843464-A.

XX

PD 01-DEC-1998.

XX

PF 02-JUN-1995; 95US-00460502.

XX

PR 02-JUN-1995; 95US-00460502.

XX

PA (OHIS) UNIV OHIO STATE.

XX

PI Kaumaya PTP, Bakaletz LO;

XX

DR WPI; 1999-044514/04.

XX

PT Synthetic chimeric fimbrin peptide - useful for vaccination against non-
PT typable Haemophilus influenzae.

XX

PS Disclosure; Col 4; 16pp; English.

XX

CC The invention relates to the manufacture of a synthetic chimeric peptide
CC comprising a non-typable Haemophilus influenzae fimbrin peptide fused via
CC a linker peptide to a T-cell epitope peptide. The chimeric peptide is
CC used in immunogenic compositions which induce an immune response against
CC non-typable Haemophilus influenzae. This sequence represents an example
CC of a T-cell epitope peptide used to generate the chimeric peptide

XX

SQ Sequence 21 AA;

Query Match 100.0%; Score 112; DB 2; Length 21;

Best Local Similarity 100.0%; Pred. No. 6.3e-12;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPKVSASHLE 21

||||||||||||||||

Db 1 FNNFTVSFWLRVPKVSASHLE 21

RESULT 7

AAW73222

ID AAW73222 standard; protein; 21 AA.

XX
 AC AAW73222;
 XX
 DT 25-JAN-1999 (first entry)
 XX
 DE Tetanus toxoid epitope.
 XX
 KW Multispecific single chain antibody; antibody H22; tumour cell; therapy;
 KW antibody-dependent cellular cytotoxicity; ADCC; HER 2/neu; infection;
 KW epidermal growth factor receptor; breast cancer; ovarian cancer.
 XX
 OS Synthetic.
 XX
 PN US5837243-A.
 XX
 PD 17-NOV-1998.
 XX
 PF 07-JUN-1996; 96US-00661052.
 XX
 PR 07-JUN-1995; 95US-00484172.
 XX
 PA (MEDA-) MEDAREX INC.
 XX
 PI Somasundaram C, Graziano R, Deo YM, Goldstein J;
 XX
 DR WPI; 1999-023374/02.
 XX
 PT Specific killing of tumour cells - using a multi-specific molecule
 PT comprising an anti-Fc receptor antibody and a portion which binds to a
 PT target cell.
 XX
 PS Example 7; Col 27; 57pp; English.
 XX
 CC This sequence represents a tetanus toxoid epitope and is recognised by
 CC the multispecific single chain antibody designated H22. The antibody can
 CC be used in the method of the invention for inducing antibody-dependent
 CC cellular cytotoxicity (ADCC) against a tumour cell which is characterised
 CC by overexpression of HER 2/neu or epidermal growth factor receptor
 CC (EGFR), comprises contacting the tumour cell with a multispecific protein
 CC molecule (preferably a single chain antibody) comprising: (a) an anti-Fc
 CC receptor antibody or an antigen binding fragment; (b) a portion which
 CC binds to HER 2/neu; and (c) a portion which binds to EGFR. The method can
 CC be used for treating cancers especially breast cancer or ovarian cancer.
 CC The multispecific antibody can also be administered prophylactically to
 CC vaccinate a subject against infection by a target cell
 XX
 SQ Sequence 21 AA;

Query Match 100.0%; Score 112; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 6.3e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSEFWLRVPKVSASHLE 21
 |||||
 Db 1 FNNFTVSEFWLRVPKVSASHLE 21

RESULT 8

AAAY92626

ID AAY92626 standard; protein; 21 AA.

XX

AC AAY92626;

XX

DT 10-AUG-2000 (first entry)

XX

DE Foreign epitope P30.

XX

KW Foreign epitope; P2; prostate specific membrane antigen; PSM; Her2;

KW Heregulin 2; Fibroblast growth factor 8b; FGF8b; vaccination;

KW cytotoxic T-lymphocyte immunity; self-protein; cancer; breast cancer;

KW prostate cancer; cell-associated peptide antigen.

XX

OS Clostridium tetani.

XX

PN WO200020027-A2.

XX

PD 13-APR-2000.

XX

PF 05-OCT-1999; 99WO-DK000525.

XX

PR 05-OCT-1998; 98DK-00001261.

PR 20-OCT-1998; 98US-0105011P.

XX

PA (MEBI-) M & E BIOTECH AS.

XX

PI Steinaa L, Mouritsen S, Nielsen KG, Haaning J, Leach D, Dalum I;

PI Gautam A, Birk P, Karlsson G;

XX

DR WPI; 2000-349917/30.

DR N-PSDB; AAA09461.

XX

PT Inducing immune responses to weakly immunogenic, tumor associated peptide
PT antigens for the treatment of breast and prostate cancer.

XX

PS Example 1; Page 214; 220pp; English.

XX

CC The claims detail a method for inducing immune responses against weakly
CC immunogenic cell-associated peptide antigens (PA) such as those
CC associated with cancers (i.e. self-proteins), for example, human prostate
CC specific membrane antigen (PSM), heregulin 2 (Her2) and/or fibroblast
CC growth factor 8b (FGF8b). The method comprises effecting simultaneous
CC presentation by antigen producing cells (APCs) of the animals immune
CC system of: (1) at least 1 CTL (cytotoxic T-lymphocyte) group derived from
CC the PA and/or at least 1 B-cell group derived from the cell-associated PA
CC ; and (2) at least 1 first T helper cell group which is foreign to the
CC animal. Analogues of human PSM, human Her2 and human/murine FGF8b
CC comprising a substantial part of all known and predicted CTL and B-cell
CC epitopes of the respective PA and including at least one foreign T helper
CC epitope (e.g. P2 and/or P30) are also claimed. The method is used to
CC treat prostate, prostate/breast or breast cancer when the PA is human
CC PSM, FGF8b and Her2, respectively

XX

SQ Sequence 21 AA;

Query Match 100.0%; Score 112; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.3e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPKVSASHLE 21
|||||
Db 1 FNNFTVSFWLRVPKVSASHLE 21

RESULT 9

AA99876

ID AA99876 standard; protein; 21 AA.

XX

AC AA99876;

XX

DT 03-OCT-2000 (first entry)

XX

DE Tetanus toxin T cell epitope helper peptide P30.

XX

KW Human; MAGE-10; tumour rejection antigen precursor; bladder cancer;

KW prostate cancer; lung cancer; cancer detection; oesophageal cancer;

KW head and neck cancer; melanoma; myeloma; sarcoma; immunogen;

KW tetanus toxin.

XX

OS Homo sapiens.

XX

PN WO200026407-A1.

XX

PD 11-MAY-2000.

XX

PF 15-OCT-1999; 99WO-US024258.

XX

PR 30-OCT-1998; 98US-00183714.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX

PI Boon-Falleur T, Brasseur F, Rimoldi D, Deplaen E;

XX

DR WPI; 2000-451624/39.

XX

PT Determining presence of cancer in samples, especially useful for

PT detecting bladder, prostate and lung cancer comprises assaying sample for

PT expression of tumor rejection antigen precursor MAGE-10.

XX

PS Example 12; Page 14; 26pp; English.

XX

CC The present sequence is a tetanus toxin T cell epitope known as Helper

CC Peptide P30. Hybrids of this peptide and an immunogenic peptide derived

CC from tumour rejection antigen precursor MAGE-10 were used to generate

CC polyclonal antiserum against MAGE-10. MAGE-10 binding monoclonal

CC antibodies can be used to detect MAGE-10 expression. A correlation

CC between MAGE-10 expression and cancer has been discovered and thus by

CC determining the presence of MAGE-10, the presence of cancer can be

CC determined. MAGE-10 expression can be detected using an immunoassay, an

CC oligonucleotide hybridisation assay or via other standard techniques.

CC This method is especially useful for determining the presence of bladder,

CC oesophageal, head and neck, prostate or lung cancer, or melanoma, myeloma

CC or sarcoma
XX
SQ Sequence 21 AA;

Query Match 100.0%; Score 112; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.3e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPKVSASHLE 21
|||||
Db 1 FNNFTVSFWLRVPKVSASHLE 21

RESULT 10

AAAY84428

ID AAY84428 standard; peptide; 21 AA.

XX

AC AAY84428;

XX

DT 25-JUL-2000 (first entry)

XX

DE Amino acid sequence of the tetanus toxoid P30 epitope.

XX

KW Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;

KW tumour necrosis factor receptor; type II transmembrane protein;

KW osteoclast differentiation; CSF-1; osteoclast activator; immune response;

KW osteoporosis; bone resorption; tetanus toxoid P30 epitope.

XX

OS Clostridium tetani.

XX

PN WO200015807-A1.

XX

PD 23-MAR-2000.

XX

PF 13-SEP-1999; 99WO-DK000481.

XX

PR 15-SEP-1998; 98DK-00001164.

PR 02-OCT-1998; 98US-0102896P.

XX

PA (MEBI-) M & E BIOTECH AS.

XX

PI Halkier T, Haaning J;

XX

DR WPI; 2000-271444/23.

XX

PT In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used to

PT treat, prevent and ameliorate osteoporosis.

XX

PS Example; Page 106; 110pp; English.

XX

CC The present sequence represents the tetanus toxoid P30 epitope. It is
CC used to create a fusion protein with murine osteoprotegerin ligand
CC (OPGL). Osteoprotegerin is a secreted member of the tumour necrosis
CC factor receptor family, which blocks osteoclastogenesis in a dose
CC dependent manner. The OPGL protein is synthesised as a type II
CC transmembrane protein. The murine and human OPGL polypeptides are 87%
CC homologous. OPGL is a potent osteoclast differentiation factor when

CC combined with CSF-1. It is not capable of inducing osteoclast
 CC differentiation in the absence of CSF-1. OPGL is also an activator of
 CC mature osteoclasts. The specification describes a method for the in vivo
 CC down-regulation of OPGL activity in an animal. The method comprises using
 CC at least one OPGL polypeptide or subsequence, and/or at least one OPGL
 CC analogue to induce an immune response in the animal. The method and OPGL
 CC polypeptide are useful for treating, preventing and ameliorating
 CC osteoporosis or other diseases or conditions characterised by excessive
 CC bone resorption
 XX
 SQ Sequence 21 AA;

Query Match 100.0%; Score 112; DB 3; Length 21;
 Best Local Similarity 100.0%; Pred. No. 6.3e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSEFWLRVPKVSASHLE 21
 |||||
 Db 1 FNNFTVSEFWLRVPKVSASHLE 21

RESULT 11

AA49260

ID AAY49260 standard; peptide; 21 AA.

XX

AC AAY49260;

XX

DT 07-FEB-2000 (first entry)

XX

DE CD4+ T cell epitope P30TT fragment.

XX

KW Carrier protein; CD4+; T cell epitope; N6; N10; N19; immunogen;

KW encapsulated bacteria.

XX

OS Synthetic.

XX

PN WO9955730-A2.

XX

PD 04-NOV-1999.

XX

PF 27-APR-1999; 99WO-IB000844.

XX

PR 27-APR-1998; 98GB-00008932.

XX

PA (CHIR-) CHIRON SPA.

XX

PI Rappuoli R, Grandi G;

XX

DR WPI; 2000-023325/02.

XX

PT Carrier proteins containing CD4+ epitopes useful for protecting against

PT diseases caused by encapsulated bacteria.

XX

PS Disclosure; Page 36; 76pp; English.

XX

CC The invention provides carrier proteins comprising at least 5 CD4+ T cell

CC epitope. The carrier protein comprises at least 1 of N6, N10 or N19. The

CC carrier protein can be prepared by expressing a vector comprising a
 CC nucleic acid molecule encoding the protein, in a host cell and recovering
 CC the expressed protein. The carrier protein can also be produced by (a)
 CC constructing oligonucleotide molecules that encode peptide epitopes; (b)
 CC annealing the oligonucleotides to form duplexes; (c) introducing the
 CC duplexes into an expression vector; (d) introducing the expression vector
 CC into a host cell; and (e) isolating the fusion protein produced from a
 CC culture of the host cells. The carrier protein can be used as a
 CC protective immunogen in the control of diseases caused by encapsulated
 CC bacteria. Sequences AAY49256-266 represent CD4+ T cell epitopes inserted
 CC in the recombinant polyepitope carrier proteins

XX

SQ Sequence 21 AA;

Query Match 100.0%; Score 112; DB 3; Length 21;
 Best Local Similarity 100.0%; Pred. No. 6.3e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPKVSASHLE 21
 |||||
 Db 1 FNNFTVSFWLRVPKVSASHLE 21

RESULT 12

AAB45512

ID AAB45512 standard; protein; 21 AA.

XX

AC AAB45512;

XX

DT 26-FEB-2001 (first entry)

XX

DE Tetanus P30 epitope SEQ ID NO: 24.

XX

KW Asthma; IL-5; interleukin-5; allergy; cytokine; helminthic infection;
 KW cancer; eosinophilia; vaccine; allergic rhinitis.

XX

OS Clostridium tetani.

XX

PN WO200065058-A1.

XX

PD 02-NOV-2000.

XX

PF 19-APR-2000; 2000WO-DK000205.

XX

PR 23-APR-1999; 99DK-00000552.

PR 06-MAY-1999; 99US-0132811P.

XX

PA (MEBI-) M & E BIOTECH AS.

XX

PI Klysner S;

XX

DR WPI; 2000-672791/65.

XX

PT Down-regulating interleukin 5 (IL-5) activity in humans by administering
 PT IL-5 and/or an IL-5 analogue, useful in the treatment, prophylaxis or
 PT amelioration of asthma or other chronic allergic conditions.

XX

PS Example 6; Page 137; 172pp; English.

XX

CC The present invention is concerned with methods of treating asthma,
CC eosinophilia, allergic rhinitis and other allergic diseases. These
CC involve the use of interleukin-5 (IL-5) analogues and modified IL-5
CC proteins and their coding sequences to down-regulate IL-5 activity and
CC thus reduce eosinophil numbers. The allergic diseases may be treated
CC using autovaccines, nucleic acid vaccines or live vaccines. In addition,
CC it is possible that they may be used in the treatment of cancer and
CC helminthic infections

XX

SQ Sequence 21 AA;

Query Match 100.0%; Score 112; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.3e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPKVSASHLE 21

|||||

Db 1 FNNFTVSFWLRVPKVSASHLE 21

RESULT 13

AAE11764

ID AAE11764 standard; peptide; 21 AA.

XX

AC AAE11764;

XX

DT 18-DEC-2001 (first entry)

XX

DE Clostridium tetani P30 epitope.

XX

KW Amyloid protein; neuroprotective; nootropic; immunostimulant; vaccine;
KW Alzheimer's disease; anticonvulsant; gene therapy; Pick's disease;
KW antidiabetic; systemic amyloidosis; maturity onset diabetes; ALS;
KW amyotrophic lateral sclerosis; Parkinson's disease; encephalopathy;
KW Huntington's disease; fronto-temporal dementia; P30 epitope.

XX

OS Clostridium tetani.

XX

PN WO200162284-A2.

XX

PD 30-AUG-2001.

XX

PF 19-FEB-2001; 2001WO-DK000113.

XX

PR 21-FEB-2000; 2000DK-00000265.

PR 01-MAR-2000; 2000US-0186295P.

XX

PA (MEBI-) M & E BIOTECH AS.

XX

PI Birk P, Jensen MR, Nielsen KG;

XX

DR WPI; 2001-589796/66.

DR N-PSDB; AAD18756.

XX

PT In vivo down-regulation of amyloid protein for the treatment of

PT Alzheimer's, comprises presenting an amyloidogenic polypeptide or its
PT subsequence and/or at least one analogue of the amyloidogenic polypeptide
PT to the immune system.

XX

PS Example 3; Page 118; 120pp; English.

XX

CC The invention relates to a method for in vivo down-regulation of amyloid
CC protein such as beta amyloid (Abeta) in an animal, including human. The
CC method comprising presenting to the animal's immune system an
CC immunogenically effective amount of at least one amyloidogenic protein or
CC its subsequence and/or at least one analogue of the amyloidogenic
CC polypeptide. The amyloidogenic protein or its subsequence, and its
CC analogue is useful for the preparation of an immunogenic composition
CC comprising an adjuvant for down-regulating amyloid in an animal. They are
CC also useful in the treatment, prophylaxis or amelioration of Alzheimer's
CC disease or other diseases characterised by amyloid deposits. They are
CC also useful in the treatment of systemic amyloidosis, maturity onset
CC diabetes, Parkinson's disease, Huntington's disease, fronto-temporal
CC dementia, amyotrophic lateral sclerosis (ALS), Pick's disease and prion-
CC related transmissible spongiform encephalopathies. They are also useful
CC for inducing production of antibodies against an amyloidogenic
CC polypeptide. The present sequence is Clostridium tetani P30 epitope
CC related to the invention

XX

SQ Sequence 21 AA;

Query Match 100.0%; Score 112; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 6.3e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| | | | | | | | | | | | | | | | | | | | |
Db 1 FNNFTVSFWLRVPKVSASHLE 21

RESULT 14

AAB49072

ID AAB49072 standard; peptide; 21 AA.

XX

AC AAB49072;

XX

DT 27-MAR-2001 (first entry)

XX

DE Tetanus toxoid TT947-967 T-cell epitope, SEQ ID NO:8.

XX

KW Amyloid disease; amyloid fibril deposition; amyloid plaque; immunogenic;
KW antibody; vaccine; Alzheimer's disease; type 2 diabetes;
KW reactive system amyloidosis; systemic senile amyloidosis;
KW familial amyloid cardiomyopathy; transmissible spongiform encephalopathy;
KW Creutzfeld-Jakob disease; Kuru;
KW haemodialysis-associated beta-2-microglobulin deposition;
KW carrier protein; universal T-cell epitope.

XX

OS Clostridium tetani.

XX

PN WO200072876-A2.

XX

PD 07-DEC-2000.
 XX
 PF 01-JUN-2000; 2000WO-US015239.
 XX
 PR 01-JUN-1999; 99US-0137010P.
 XX
 PA (NEUR-) NEURALAB LTD.
 XX
 PI Schenk DB;
 XX
 DR WPI; 2001-070921/08.
 XX
 PT Pharmaceutical composition comprising immunogen against amyloid component
 PT such as fibril peptide or protein, or antibody against amyloid component
 PT useful for treating amyloid diseases or amyloidoses.
 XX
 PS Disclosure; Page 43; 140pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition for
 CC preventing or treating a disease characterised by amyloid fibril deposits
 CC (amyloid plaques) in a patient. The pharmaceutical composition comprises
 CC an agent that will induce an immune response against an amyloid
 CC component, or an antibody or antibody fragment that binds to an amyloid
 CC component. The invention also relates to a method for determining the
 CC prognosis of a patient undergoing treatment for an amyloid disorder which
 CC involves measuring a patient serum amount of immunoreactivity against a
 CC selected amyloid component. A patient serum immunoreactivity of at least
 CC four times a base line serum immunoreactivity control level indicates a
 CC prognosis of improved status with respect to the disorder. The
 CC pharmaceutical compositions of the invention are useful for treating a
 CC wide variety of disorders characterised by amyloid fibril deposition in a
 CC patient. Such disorders include Alzheimer's disease characterised by
 CC amyloid beta peptide fibril deposits; type 2 diabetes characterised by
 CC islet amyloid protein peptide (IAPP, amylin) fibrils; reactive systemic
 CC amyloidosis associated with systemic inflammatory diseases (e.g.,
 CC rheumatoid arthritis, osteomyelitis, tuberculosis) characterised by AA
 CC fibrils derived from serum amyloid A protein (ApoSSA)); systemic senile
 CC amyloidosis and familial amyloid cardiomyopathy characterised by ATTR
 CC fibrils derived from transthyretin (TTR); transmissible spongiform
 CC encephalopathies (e.g. Creutzfeld-Jakob disease, Kuru) characterised by
 CC prion protein deposits; and beta-2-microglobulin deposits which form as a
 CC result of long term haemodialysis treatment. The present sequence
 CC represents a universal T-cell epitope which may be used as a carrier for
 CC an epitope derived from an amyloid plaque component in a composition of
 CC the invention
 XX
 SQ Sequence 21 AA;

Query Match 100.0%; Score 112; DB 4; Length 21;
 Best Local Similarity 100.0%; Pred. No. 6.3e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPKVSASHLE 21
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 Db 1 FNNFTVSFWLRVPKVSASHLE 21

RESULT 15

AAB46173

ID AAB46173 standard; peptide; 21 AA.

XX

AC AAB46173;

XX

DT 04-APR-2001 (first entry)

XX

DE Tetanus toxoid TT947-967 epitope.

XX

KW Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;

KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;

KW amyloid precursor protein; Alzheimer's disease.

XX

OS Clostridium tetani.

XX

PN WO200072880-A2.

XX

PD 07-DEC-2000.

XX

PF 26-MAY-2000; 2000WO-US014810.

XX

PR 28-MAY-1999; 99US-00322289.

XX

PA (NEUR-) NEURALAB LTD.

XX

PI Schenk DB, Bard F, Vasquez NJ, Yednock T;

XX

DR WPI; 2001-032104/04.

XX

PT Preventing or treating a disease associated with amyloid deposits,
PT especially Alzheimer's disease, comprises administering amyloid specific
PT antibody.

XX

PS Disclosure; Page 28; 143pp; English.

XX

CC This invention describes a novel method of preventing or treating a
CC disease associated with amyloid deposits of amyloid precursor protein
CC (APP) Abeta fragments in the brain of a patient, which comprises
CC administering to the patient: (a) an antibody that binds to Abeta, the
CC antibody binds to an amyloid deposit and induces a clearing response (Fc
CC receptor mediated phagocytosis) against it (b) a polypeptide containing
CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
CC that induces an immunogenic response against residues 1-3 to 7-11 of
CC Abeta. The products of the invention have nootropic and neuroprotective
CC activity. The method is also useful for monitoring a course of treatment
CC being administered to a patient e.g. active and passive immunization. The
CC methods are useful for prophylactic and therapeutic treatment of
CC Alzheimer's disease

XX

SQ Sequence 21 AA;

Query Match 100.0%; Score 112; DB 4; Length 21;

Best Local Similarity 100.0%; Pred. No. 6.3e-12;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Job time : 5.74359 secs

OM protein - protein search, using sw model

Run on: August 13, 2004, 09:09:23 ; Search time 1.4359 Seconds
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Title: US-09-785-215-6
Perfect score: 112
Sequence: 1 FNNFTVSEFWLRVPKVSASHLE 21

Scoring table: BLOSUM62
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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Match	Length			
1	112	100.0	21	1	US-07-610-525-1	Sequence 1, Appli
2	112	100.0	21	2	US-08-661-052-12	Sequence 12, Appl
3	112	100.0	21	2	US-08-460-502-8	Sequence 8, Appli
4	112	100.0	21	2	US-08-724-774B-5	Sequence 5, Appli
5	112	100.0	21	3	US-09-089-595-5	Sequence 5, Appli
6	112	100.0	21	3	US-09-382-855-5	Sequence 5, Appli
7	112	100.0	21	3	US-09-183-714B-5	Sequence 5, Appli
8	112	100.0	21	3	US-09-188-082-12	Sequence 12, Appl
9	112	100.0	21	3	US-09-171-969-10	Sequence 10, Appl
10	112	100.0	21	4	US-09-364-088-12	Sequence 12, Appl
11	112	100.0	21	4	US-09-642-281-5	Sequence 5, Appli

12	112	100.0	21	4	US-09-102-716-12	Sequence 12, Appl
13	112	100.0	21	4	US-08-432-483A-3	Sequence 3, Appli
14	112	100.0	21	4	US-09-148-711A-8	Sequence 8, Appli
15	112	100.0	21	4	US-09-589-717-5	Sequence 5, Appli
16	112	100.0	21	4	US-08-945-289-3	Sequence 3, Appli
17	112	100.0	21	4	US-09-396-937-35	Sequence 35, Appl
18	112	100.0	21	4	US-09-405-986A-2	Sequence 2, Appli
19	112	100.0	21	5	PCT-US93-11703-66	Sequence 66, Appl
20	112	100.0	31	5	PCT-US93-11703-64	Sequence 64, Appl
21	112	100.0	32	1	US-08-446-692-14	Sequence 14, Appl
22	112	100.0	32	2	US-08-488-351A-14	Sequence 14, Appl
23	112	100.0	173	4	US-09-396-937-20	Sequence 20, Appl
24	112	100.0	188	4	US-09-396-937-14	Sequence 14, Appl
25	112	100.0	452	1	US-07-618-312A-2	Sequence 2, Appli
26	112	100.0	452	1	US-07-618-312A-4	Sequence 4, Appli
27	112	100.0	452	1	US-08-110-786A-8	Sequence 8, Appli
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29	112	100.0	452	1	US-08-280-228-4	Sequence 4, Appli
30	112	100.0	618	1	US-08-668-381A-5	Sequence 5, Appli
31	112	100.0	853	4	US-08-913-880C-17	Sequence 17, Appl
32	112	100.0	858	4	US-08-913-880C-16	Sequence 16, Appl
33	112	100.0	860	4	US-08-913-880C-15	Sequence 15, Appl
34	112	100.0	862	4	US-08-913-880C-14	Sequence 14, Appl
35	112	100.0	865	4	US-08-913-880C-13	Sequence 13, Appl
36	112	100.0	866	4	US-08-913-880C-12	Sequence 12, Appl
37	112	100.0	874	4	US-08-913-880C-11	Sequence 11, Appl
38	112	100.0	875	4	US-08-913-880C-10	Sequence 10, Appl
39	112	100.0	1315	4	US-08-913-880C-1	Sequence 1, Appli
40	107	95.5	22	1	US-08-446-692-5	Sequence 5, Appli
41	107	95.5	22	2	US-08-488-351A-5	Sequence 5, Appli
42	107	95.5	22	3	US-09-100-409A-41	Sequence 41, Appl
43	107	95.5	22	5	PCT-US95-13841-8	Sequence 8, Appli
44	100	89.3	19	1	US-07-610-525-2	Sequence 2, Appli
45	94.5	84.4	20	2	US-08-319-704-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-07-610-525-1

; Sequence 1, Application US/07610525

; Patent No. 5196512

; GENERAL INFORMATION:

; APPLICANT: BIANCHI Eisabetta

; APPLICANT: PESSI Antonello

; APPLICANT: CORRADIN Giampietro

; TITLE OF INVENTION: SYNTHETIC PEPTIDES USEFUL AS

; TITLE OF INVENTION: UNIVERSAL CARRIERS FOR THE PREPARATION OF IMMUNOGENIC CONJUGATES

; TITLE OF INVENTION: AND THEIR USE IN THE DEVELOPMENT OF SYNTHETIC VACCINES.

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SHEA & GOULD

; STREET: 1251 AVENUE OF THE AMERICAS

; CITY: NEW YORK

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; STATE: NEW YORK
; COUNTRY: UNITED STATES
; ZIP: 10020-1193
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/610,525
; FILING DATE: 19901108
; CLASSIFICATION: 424
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-827-3000
; TELEFAX: 212-840-6702
; TELEX: 423973
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acid residues
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: no
; FRAGMENT TYPE: internal fragment
US-07-610-525-1

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Query Match          100.0%; Score 112; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 FNNFTVSFWLRVPKVSASHLE 21

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RESULT 2

US-08-661-052-12

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; Sequence 12, Application US/08661052
; Patent No. 5837243

```

GENERAL INFORMATION:

```

; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; TITLE OF INVENTION: OF ANTI-Fc RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/661,052
;     FILING DATE:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/484,172
;     FILING DATE:  07-JUNE-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Arnold, Beth E.
;     REGISTRATION NUMBER:  35,430
;     REFERENCE/DOCKET NUMBER:  MXI-043CP
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (617)227-7400
;     TELEFAX:  (617)227-5941
;   INFORMATION FOR SEQ ID NO:  12:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  21 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     FRAGMENT TYPE:  internal
US-08-661-052-12

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Best Local Similarity 100.0%;  Pred. No. 2.2e-12;
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RESULT 3

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US-08-460-502-8
; Sequence 8, Application US/08460502
; Patent No. 5843464
; GENERAL INFORMATION:
;   APPLICANT:  Bakaletz, Lauren O.
;   APPLICANT:  Kaumaya, Parvin T.
;   TITLE OF INVENTION:  Synthetic Chimeric Fimbrin Peptides
;   NUMBER OF SEQUENCES:  11
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Calfee, Halter and Griswold
;     STREET:  800 Superior Avenue
;     CITY:  Cleveland
;     STATE:  Ohio
;     COUNTRY:  U.S.A.
;     ZIP:  44114-2688
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/460,502

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; FILING DATE:
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Golrick, Mary E.
 ; REGISTRATION NUMBER: 34,829
 ; REFERENCE/DOCKET NUMBER: 22727/00120
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (216) 622-8458
 ; TELEFAX: (216) 241-0816
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 21 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-460-502-8

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 Best Local Similarity 100.0%; Pred. No. 2.2e-12;
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 Db 1 FNNFTVSFWLRVPKVSASHLE 21

RESULT 4

US-08-724-774B-5

; Sequence 5, Application US/08724774B
 ; Patent No. 5908778
 ; GENERAL INFORMATION:
 ; APPLICANT: Rimoldi, Donata; Jongeneel, Victor; Coulie,
 ; APPLICANT: Pierre; Cerrottini, Jean-Charles; Carrel,
 ; APPLICANT: Stefan; Reed, Daryl
 ; TITLE OF INVENTION: MAGE-10 ENCODING cDNA, The Tumor
 ; TITLE OF INVENTION: Rejection Antigen Precuros Mage-10,
 ; TITLE OF INVENTION: Antibodies Specific To The Molecule, and
 ; TITLE OF INVENTION: Uses Thereof
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Felfe & Lynch
 ; STREET: 805 Third Avenue
 ; CITY: New York City
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10022
 ; COMPUTER READABLE FORM:
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 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: Wordperfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/724,774B
 ; FILING DATE: 03-October-1996
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:

; NAME: Hanson, No. 5908778man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5457
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: amino acid
; TOPOLOGY: linear
US-08-724-774B-5

Query Match 100.0%; Score 112; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPKVSASHLE 21
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RESULT 5

US-09-089-595-5

; Sequence 5, Application US/09089595
; Patent No. 6153728
; GENERAL INFORMATION:
; APPLICANT: Rimoldi, Donata; Jongeneel, Victor; Coulie,
; APPLICANT: Pierre; Cerrottini, Jean-Charles; Carrel,
; APPLICANT: Stefan; Reed, Daryl
; TITLE OF INVENTION: MAGE-10 ENCODING cDNA, The Tumor
; TITLE OF INVENTION: Rejection Antigen Precuros Mage-10,
; TITLE OF INVENTION: Antibodies Specific To The Molecule, and
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
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; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
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; APPLICATION NUMBER: US/09/089,595
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,774
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6153728man D.
; REGISTRATION NUMBER: 30,946

; REFERENCE/DOCKET NUMBER: LUD 5457
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: amino acid
; TOPOLOGY: linear
US-09-089-595-5

Query Match 100.0%; Score 112; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSEFWLRVPKVSASHLE 21
|||||
Db 1 FNNFTVSEFWLRVPKVSASHLE 21

RESULT 6

US-09-382-855-5

; Sequence 5, Application US/09382855
; Patent No. 6174692

; GENERAL INFORMATION:

; APPLICANT: Rimoldi, Donata; Jongeneel, Victor; Coulie, Pierre;
; APPLICANT: Cerrottini, Jean-Charles; Carrel, Stefan; Reed, Daryl
; TITLE OF INVENTION: MAGE-10 ENCODING cDNA, The Tumor Rejection
; TITLE OF INVENTION: Antigen Precuros Mage-10, Antibodies Specific To The
Molecule, a

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fulbright & Jaworski LLP

; STREET: 666 Fifth Avenue

; CITY: New York City

; STATE: New York

; COUNTRY: USA

; ZIP: 10103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage

; COMPUTER: IBM

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/382,855

; FILING DATE: 25-August-1999

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 09/089,595

; FILING DATE: 02-June-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/724,774

; FILING DATE: 03-October-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Schofield, Mary Anne

; REGISTRATION NUMBER: 36,669

; REFERENCE/DOCKET NUMBER: LUD 5457.2 DIV - JEL/MAS

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: amino acid
; TOPOLOGY: linear
US-09-382-855-5

Query Match 100.0%; Score 112; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPKVSASHLE 21
|||||
Db 1 FNNFTVSFWLRVPKVSASHLE 21

RESULT 7

US-09-183-714B-5

; Sequence 5, Application US/09183714B
; Patent No. 6221593
; GENERAL INFORMATION:
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Brasseur, Francis
; APPLICANT: Rimoldi, Donata
; APPLICANT: De Plaen, Etienne
; TITLE OF INVENTION: Method for Determining Cancer by Determining Expression
; TITLE OF INVENTION: of MAGE-10
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/183,714B
; CURRENT FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: US 08/724,774
; PRIOR FILING DATE: 1996-10-03
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 5
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-183-714B-5

Query Match 100.0%; Score 112; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPKVSASHLE 21
|||||
Db 1 FNNFTVSFWLRVPKVSASHLE 21

RESULT 8

US-09-188-082-12

; Sequence 12, Application US/09188082
; Patent No. 6270765
; GENERAL INFORMATION:

```

; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; TITLE OF INVENTION: OF ANTI-Fc RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/188,082
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/661,052
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-188-082-12

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Query Match          100.0%; Score 112; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 FNNFTVSFWLRVPKVSASHLE 21
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Db      1 FNNFTVSFWLRVPKVSASHLE 21

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RESULT 9

US-09-171-969-10

; Sequence 10, Application US/09171969

; Patent No. 6284533

; GENERAL INFORMATION:

; APPLICANT: Thomas, Lawrence J.

; TITLE OF INVENTION: PLASMID-BASED VACCINE FOR TREATING ATHEROSCLEROSIS

```

; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 75 State Street, Suite 2300
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1807
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/171,969
; FILING DATE: 01 May 1997 (01.05.97)
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/640,713
; FILING DATE: 01 May 1996 (01.05.96)
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/802,967
; FILING DATE: 21 February 1997 (21.02.97)
; ATTORNEY/AGENT INFORMATION:
; NAME: Leon R. Yankwich
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: TCS 414.1 PCT (05872)
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL:
; ANTI-SENSE:
; FEATURE:
; NAME/KEY:
; LOCATION:
US-09-171-969-10

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Query Match          100.0%; Score 112; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 FNNFTVSFWLRVPKVSASHLE 21
        ||||||||||||||||
Db      1 FNNFTVSFWLRVPKVSASHLE 21

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RESULT 10
US-09-364-088-12
; Sequence 12, Application US/09364088
; Patent No. 6365161
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo, et al.
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; TITLE OF INVENTION: OF ANTI-Fc RECEPTOR ANTIBODIES

```

; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; STREET: 28 State Street, 24th Floor
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/364,088
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 09/188,082
 ; FILING DATE: 07-JUNE-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/484,172
 ; FILING DATE: 07-JUNE-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Remillard, Jane E.
 ; REGISTRATION NUMBER: 38,872
 ; REFERENCE/DOCKET NUMBER: MXI-043CP2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)742-7414
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 21 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: internal
 US-09-364-088-12

Query Match 100.0%; Score 112; DB 4; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.2e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPKVSASHLE 21
 |||||
 Db 1 FNNFTVSFWLRVPKVSASHLE 21

RESULT 11

US-09-642-281-5

; Sequence 5, Application US/09642281
 ; Patent No. 6387698

GENERAL INFORMATION:

; APPLICANT: Rimoldi, Donata; Jongeneel, Victor; Coulie, Pierre;
 ; Cerrottini, Jean-Charles; Carrel, Stefan; Reed, Daryl
 ; TITLE OF INVENTION: MAGE-10 ENCODING cDNA, The Tumor Rejection
 ; Antigen Precuros Mage-10, Antibodies Specific To
 The Molecule, and Uses Thereof

; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fulbright & Jaworski LLP
 ; STREET: 666 Fifth Avenue
 ; CITY: New York City
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10103
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
 ; COMPUTER: IBM
 ; OPERATING SYSTEM: PC-DOS
 ; SOFTWARE: Wordperfect
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/642,281
 ; FILING DATE: 18-Aug-2000
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 09/089,595
 ; FILING DATE: 02-June-1998
 ; APPLICATION NUMBER: US 08/724,774
 ; FILING DATE: 03-October-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Schofield, Mary Anne
 ; REGISTRATION NUMBER: 36,669
 ; REFERENCE/DOCKET NUMBER: LUD 5457.2 DIV - JEL/MAS
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 318-3000
 ; TELEFAX: (212) 752-5958
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 21
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 US-09-642-281-5

Query Match 100.0%; Score 112; DB 4; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.2e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNNFTVSFWLRVPKVSASHLE 21
 |||||
 Db 1 FNNFTVSFWLRVPKVSASHLE 21

RESULT 12
 US-09-102-716-12
 ; Sequence 12, Application US/09102716
 ; Patent No. 6395272
 ; GENERAL INFORMATION:
 ; APPLICANT: Yashwant M. Deo
 ; Joel Goldstein
 ; Robert Graziano
 ; Chezian Somasundaram
 ; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
 ; OF ANTI-Fc RECEPTOR ANTIBODIES

```

;      NUMBER OF SEQUENCES: 16
;      CORRESPONDENCE ADDRESS:
;      ADDRESSEE: LAHIVE & COCKFIELD
;      STREET: 60 State Street, Suite 510
;      CITY: Boston
;      STATE: Massachusetts
;      COUNTRY: USA
;      ZIP: 02109-1875
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.25
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/102,716
;      FILING DATE: 22-Jun-1998
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 08/661,052
;      FILING DATE: <Unknown>
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Arnold, Beth E.
;      REGISTRATION NUMBER: 35,430
;      REFERENCE/DOCKET NUMBER: MXI-043CP
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (617)227-7400
;      TELEFAX: (617)227-5941
;      INFORMATION FOR SEQ ID NO: 12:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 21 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: peptide
;      FRAGMENT TYPE: internal
;      SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-102-716-12

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Query Match          100.0%; Score 112; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 FNNFTVSFWLRVPKVSASHLE 21
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Db      1 FNNFTVSFWLRVPKVSASHLE 21

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RESULT 13

US-08-432-483A-3

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; Sequence 3, Application US/08432483A
; Patent No. 6410022

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GENERAL INFORMATION:

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; APPLICANT: Rittershaus, Charles W.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
; TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: Ten South Wacker Drive

```



```

; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-7407
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/432,483A
; FILING DATE: 1-May-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Leon R. Yankwich
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: 95,179 (TCS-95179)
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL:
; ANTI-SENSE:
; FEATURE:
; NAME/KEY: 21-amino acid tetanus toxoid universal
; NAME/KEY: helper T cell epitope.
; LOCATION:
; PUBLICATION INFORMATION:
; AUTHORS: Panina-Bordignon, P., et al.
; TITLE: Universally immunogenic T cell
; TITLE: epitopes: promiscuous binding to human MHC class II and
; TITLE: promiscuous recognition by T cells
; JOURNAL: European Journal of Immunology
; VOLUME: 19
; ISSUE:
; PAGES: 2237-2242
; DATE: 1989
; RELEVANT RESIDUES IN SEQ ID NO: 3: FROM 1 TO 21
US-08-432-483A-3

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Query Match          100.0%; Score 112; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 FNNFTVSFWLRVPKVSASHLE 21
        |||
Db      1 FNNFTVSFWLRVPKVSASHLE 21

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RESULT 14
US-09-148-711A-8
; Sequence 8, Application US/09148711A

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; Patent No. 6436405
; GENERAL INFORMATION:
; APPLICANT: The Ohio State University
; TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides
; FILE REFERENCE: 18525-04010
; CURRENT APPLICATION NUMBER: US/09/148,711A
; CURRENT FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 08/460,502
; PRIOR FILING DATE: 1995-06-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 21
; TYPE: PRT
; ORGANISM: clostridium tetani
US-09-148-711A-8

Query Match 100.0%; Score 112; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSEFWLRVPKVSASHLE 21
|||||
Db 1 FNNFTVSEFWLRVPKVSASHLE 21

RESULT 15

US-09-589-717-5

; Sequence 5, Application US/09589717
; Patent No. 6497879
; GENERAL INFORMATION:
; APPLICANT: Rimoldi, Donata; Jongeneel, Victor; Coulie,
; Pierre; Cerrottini, Jean-Charles; Carrel,
; Stefan; Reed, Daryl
; TITLE OF INVENTION: MAGE-10 ENCODING cDNA, The Tumor
; Rejection Antigen Precuros Mage-10,
; Antibodies Specific To The Molecule, and
; Uses Thereof
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/589,717
; FILING DATE: 08-Jun-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/089,595

; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6497879man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5457
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-589-717-5

Query Match 100.0%; Score 112; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2e-12;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPKVSASHLE 21
| | | | | | | | | | | | | | | | | | | | | |
Db 1 FNNFTVSFWLRVPKVSASHLE 21

Search completed: August 13, 2004, 09:17:36
Job time : 2.4359 secs

OM protein - protein search, using sw model

Run on: August 13, 2004, 09:08:23 ; Search time 1.15385 Seconds
(without alignments)
1750.686 Million cell updates/sec

Title: US-09-785-215-6
Perfect score: 112
Sequence: 1 FNNFTVSFWLRVPKVSASHLE 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	112	100.0	1315	1	BTCLTN	tentoxilysin (EC 3
2	62	55.4	1268	2	S33411	botulinum neurotox
3	61	54.5	366	2	S48110	neurotoxin type F
4	61	54.5	369	2	S48109	neurotoxin type F
5	61	54.5	1274	2	I40813	neurotoxin type F
6	61	54.5	1297	2	S39791	neurotoxin - Clost
7	59	52.7	1296	1	BTCLAB	bontoxilysin (EC 3
8	58	51.8	1291	1	A48940	bontoxilysin (EC 3
9	58	51.8	1291	2	I40631	non-proteolytic bo
10	56	50.0	367	2	S48106	neurotoxin type E
11	56	50.0	1251	2	JH0256	botulinum neurotox
12	56	50.0	1252	2	S21178	botulinum neurotox
13	56	50.0	1296	2	I40645	botulinum neurotox

14	52	46.4	449	2	S23158	nucleocapsid prote
15	52	46.4	464	1	MNVUWC	nonstructural prot
16	52	46.4	467	1	MNVUW1	nonstructural prot
17	51	45.5	1196	2	JQ1467	toxin, nontoxic co
18	51	45.5	1196	2	S46430	botulinum neurotox
19	49	43.8	276	2	T33493	hypothetical prote
20	48	42.9	504	2	T47446	hypothetical prote
21	48	42.9	1285	2	S70582	botulinum neurotox
22	48	42.9	1291	2	S46431	botulinum neurotox
23	48	42.9	1291	2	A49777	botulinum neurotox
24	47.5	42.4	1276	2	S11455	botulinum neurotox
25	47	42.0	359	2	F87937	protein F14B6.6 [i
26	47	42.0	385	2	T20879	hypothetical prote
27	47	42.0	469	2	B37837	probable alpha-amy
28	46	41.1	322	2	T25966	hypothetical prote
29	46	41.1	442	2	I47074	gene CD5 protein -
30	46	41.1	496	2	T38197	probable myb-like
31	46	41.1	753	2	C96668	unknown protein F1
32	46	41.1	1162	2	A47708	progenitor toxin n
33	46	41.1	1162	2	I40817	botulinum toxin no
34	45	40.2	528	2	T41362	hypothetical prote
35	45	40.2	886	2	T39081	hypothetical prote
36	44	39.3	209	2	A82470	conserved hypothet
37	44	39.3	404	2	AD0574	enterochelin ester
38	44	39.3	591	2	S04401	spheroidene monoox
39	43	38.4	152	2	D64943	probable membrane
40	43	38.4	152	2	B99945	hypothetical prote
41	43	38.4	152	2	E85793	hypothetical prote
42	43	38.4	381	2	A90711	hypothetical prote
43	43	38.4	381	2	E85561	hypothetical prote
44	43	38.4	514	2	T20858	hypothetical prote
45	43	38.4	781	2	F83884	hypothetical prote

ALIGNMENTS

RESULT 1

BTCLTN

tentoxilysin (EC 3.4.24.68) precursor - Clostridium tetani

N;Alternate names: tetanus neurotoxin

C;Species: Clostridium tetani

C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 03-Jun-2002

C;Accession: A25689; A25757; A25194; B25194; A60759; S69348; S09364

R;Eisel, U.; Jarausch, W.; Goretzki, K.; Henschen, A.; Engels, J.; Weller, U.; Hudel, M.; Habermann, E.; Niemann, H.

EMBO J. 5, 2495-2502, 1986

A;Title: Tetanus toxin: primary structure, expression in E. coli, and homology with botulinum toxins.

A;Reference number: A25689; MUID:87053814; PMID:3536478

A;Accession: A25689

A;Molecule type: DNA

A;Residues: 1-1315 <EIS>

A;Cross-references: GB:X04436; NID:g40769; PIDN:CAA28033.1; PID:g40770

R;Fairweather, N.F.; Lyness, V.A.

Nucleic Acids Res. 14, 7809-7812, 1986

A;Title: The complete nucleotide sequence of tetanus toxin.

A;Reference number: A25757; MUID:87040747; PMID:3774547
 A;Accession: A25757
 A;Molecule type: DNA
 A;Residues: 1-1315 <FAI>
 A;Cross-references: GB:X06214; NID:g40773; PIDN:CAA29564.1; PID:g40774
 A;Experimental source: strain CN3911
 R;Fairweather, N.F.; Lyness, V.A.; Pickard, D.J.; Allen, G.; Thomson, R.O.
 J. Bacteriol. 165, 21-27, 1986
 A;Title: Cloning, nucleotide sequencing, and expression of tetanus toxin
 fragment C in Escherichia coli.
 A;Reference number: A25194; MUID:86085672; PMID:3510187
 A;Accession: A25194
 A;Molecule type: DNA
 A;Residues: 743-1315 <FA2>
 A;Cross-references: GB:M12739; NID:g144920; PIDN:AAA23282.1; PID:g144921
 A;Accession: B25194
 A;Molecule type: protein
 A;Residues: 865-894 <FA3>
 R;Matsuda, M.; Lei, D.L.; Sugimoto, N.; Ozutsumi, K.; Okabe, T.
 Infect. Immun. 57, 3588-3593, 1989
 A;Title: Isolation, purification, and characterization of fragment B, the NH-2-
 terminal half of the heavy chain of tetanus toxin.
 A;Reference number: A60759; MUID:90035436; PMID:2478476
 A;Accession: A60759
 A;Molecule type: protein
 A;Residues: 461-475 <MAT>
 R;Demotz, S.; Lanzavecchia, L.; Eisel, U.; Niemann, H.; Widmann, C.; Corradin,
 G.
 J. Immunol. 142, 394-402, 1989
 A;Title: Delineation of several DR-restricted tetanus toxin T cell epitopes.
 A;Reference number: JS0098; MUID:89093918; PMID:2463305
 A;Contents: annotation; epitope region
 R;Schiavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.;
 DasGupta, B.R.; Montecucco, C.
 Nature 359, 832-835, 1992
 A;Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by
 proteolytic cleavage of synaptobrevin.
 A;Reference number: S27125; MUID:93063293; PMID:1331807
 A;Contents: annotation
 R;de Filippis, V.; Vangelista, L.; Schiavo, G.; Tonello, F.; Montecucco, C.
 Eur. J. Biochem. 229, 61-69, 1995
 A;Title: Structural studies on the zinc-endopeptidase light chain of tetanus
 neurotoxin.
 A;Reference number: S69348; MUID:95262688; PMID:7744050
 A;Accession: S69348
 A;Molecule type: protein
 A;Residues: 2-31 <DEF>
 C;Comment: The source of this protein was an extrachromosomal plasmid.
 C;Comment: The precursor is cleaved by endogenous proteinase activity to form
 light (fragment A) and heavy (fragment B.C) chains that are covalently linked by
 an interchain disulfide bond (the individual chains are not toxic when
 separated). The amino end of the heavy chain (fragment B) can be separated from
 the carboxyl end (fragment C) by papain.
 C;Comment: Fragment B forms ion channels in a lipid bilayer. Fragment C binds to
 gangliosides and may target the toxin to the motor end plate. Fragment A is a
 zinc-dependent endopeptidase.

C;Comment: This potent neurotoxin binds to peripheral neuronal synapses, is internalized, and moves by retrograde transport up the axon into the spinal cord where it can move between postsynaptic and presynaptic neurons. It inhibits neurotransmitter release by proteolytic cleavage of synaptobrevin (vesicle-associated membrane protein 2).

C;Function:

A;Description: blocks neuroexocytosis via hydrolysis of a Gln-Phe peptide bond in synaptobrevin 2

C;Superfamily: tetanus toxin

C;Keywords: hydrolase; metalloproteinase; neurotoxin; transmembrane protein; zinc

F;2-457/Product: tentoxylisin light chain (fragment A) #status predicted <TTL>

F;461-1315/Product: tentoxylisin heavy chain (fragment B.C) #status experimental <TTH>

F;461-864/Domain: channel forming (fragment B) #status predicted <TXB>

F;865-1315/Domain: ganglioside binding (fragment C) #status predicted <TXC>

F;233,237/Binding site: zinc (His) #status predicted

F;234/Active site: Glu #status predicted

Query Match 100.0%; Score 112; DB 1; Length 1315;
Best Local Similarity 100.0%; Pred. No. 3.6e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSEFWLRVPKVSASHLE 21
| | | | | | | | | | | | | | | | | | | | |
Db 947 FNNFTVSEFWLRVPKVSASHLE 967

RESULT 2

S33411

botulinum neurotoxin type F - Clostridium barati

C;Species: Clostridium barati

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999

C;Accession: S33411; S31860

R;Thompson, D.E.; Hutson, R.A.; East, A.K.; Allaway, D.; Collins, M.D.; Richardson, P.T.

FEMS Microbiol. Lett. 108, 175-182, 1993

A;Title: Nucleotide sequence of the gene coding for Clostridium barati type F neurotoxin: comparison with other clostridial neurotoxins.

A;Reference number: S33411; MUID:93252228; PMID:8486245

A;Accession: S33411

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1268 <THO>

A;Cross-references: EMBL:X68262; NID:g49138; PIDN:CAA48329.1; PID:g49139

C;Superfamily: tetanus toxin

C;Keywords: neurotoxin

Query Match 55.4%; Score 62; DB 2; Length 1268;
Best Local Similarity 64.3%; Pred. No. 0.073;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FNNFTVSEFWLRVPK 14
: ||:||||:|:|
Db 922 YQNFSVSEFWVRIPK 935

RESULT 3

S48110

neurotoxin type F - Clostridium botulinum (fragment)

C;Species: Clostridium botulinum

C;Date: 14-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999

C;Accession: S48110

R;Campbell, K.D.; Collins, M.D.; East, A.K.

J. Clin. Microbiol. 31, 2255-2262, 1993

A;Title: Gene probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F.

A;Reference number: S48103; MUID:94013372; PMID:8408542

A;Accession: S48110

A;Status: preliminary; translation not shown

A;Molecule type: DNA

A;Residues: 1-366 <CAM>

A;Cross-references: EMBL:X70821; NID:g407792; PIDN:CAA50152.1; PID:g407793

C;Superfamily: tetanus toxin

C;Keywords: neurotoxin

Query Match 54.5%; Score 61; DB 2; Length 366;
Best Local Similarity 57.1%; Pred. No. 0.028;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPK 14
: ||::|||:|:|
Db 297 YQNFSISFWVRIPK 310

RESULT 4

S48109

neurotoxin type F - Clostridium botulinum (fragment)

C;Species: Clostridium botulinum

C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 16-Jul-1999

C;Accession: S48109

R;Campbell, K.D.; Collins, M.D.; East, A.K.

J. Clin. Microbiol. 31, 2255-2262, 1993

A;Title: Gene probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F.

A;Reference number: S48103; MUID:94013372; PMID:8408542

A;Accession: S48109

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-369 <CAM>

A;Cross-references: EMBL:X70820; NID:g407790; PIDN:CAA50151.1; PID:g407791

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993

C;Superfamily: tetanus toxin

Query Match 54.5%; Score 61; DB 2; Length 369;
Best Local Similarity 57.1%; Pred. No. 0.029;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPK 14
: ||::|||:|:|
Db 297 YQNFSISFWVRIPK 310

RESULT 5

I40813

neurotoxin type F - Clostridium botulinum

C;Species: Clostridium botulinum

C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Jul-1999

C;Accession: I40813; S48108

R;East, A.K.; Richardson, P.T.; Allaway, D.; Collins, M.D.; Roberts, T.A.; Thompson, D.E.

FEMS Microbiol. Lett. 96, 225-230, 1992

A;Title: Sequence of the gene encoding type F neurotoxin of Clostridium botulinum.

A;Reference number: I40644

A;Accession: I40813

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1274 <RES>

A;Cross-references: GB:M92906; NID:g144866; PIDN:AAA23263.1; PID:g144867

R;Campbell, K.D.; Collins, M.D.; East, A.K.

J. Clin. Microbiol. 31, 2255-2262, 1993

A;Title: Gene probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F.

A;Reference number: S48103; MUID:94013372; PMID:8408542

A;Accession: S48108

A;Status: preliminary; translation not shown

A;Molecule type: DNA

A;Residues: 634-1002 <CAM>

A;Cross-references: EMBL:X70816; NID:g407788; PIDN:CAA50147.1; PID:g407789

C;Superfamily: tetanus toxin

C;Keywords: neurotoxin

Query Match 54.5%; Score 61; DB 2; Length 1274;
Best Local Similarity 57.1%; Pred. No. 0.11;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FNNFTVSEFWLRVPK 14
: ||::|||:|:|
Db 930 YQNFSISFWVRIPK 943

RESULT 6

S39791

neurotoxin - Clostridium botulinum

C;Species: Clostridium botulinum

C;Date: 07-Oct-1994 #sequence_revision 01-Dec-1995 #text_change 16-Jul-1999

C;Accession: S39791

R;Campbell, K.; Collins, M.D.; East, A.K.

Biochim. Biophys. Acta 1216, 487-491, 1993

A;Title: Nucleotide sequence of the gene coding for Clostridium botulinum (Clostridium argentinense) type G neurotoxin: genealogical comparison with other clostridial neurotoxins.

A;Reference number: S39791; MUID:94092745; PMID:8268233

A;Accession: S39791

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1297 <CAM>

A;Cross-references: EMBL:X74162; NID:g441275; PIDN:CAA52275.1; PID:g441276

C;Superfamily: tetanus toxin

C;Keywords: neurotoxin

Query Match 54.5%; Score 61; DB 2; Length 1297;
Best Local Similarity 38.1%; Pred. No. 0.11;
Matches 8; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

```

Qy          1 FNNFTVSFWLRVPKVSASHLE 21
              |:|:|:|:|:|:| | | : : : :
Db        930 EDNFSINFVWVRTPKYNNNDIO 950

```

RESULT 7

BTCLAB

bontoxilysin (EC 3.4.24.69) A precursor - Clostridium botulinum

N; Alternate names: botulinum neurotoxin type A

C;Species: Clostridium botulinum

C;Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text change 18-Jun-1999

C;Accession: A35294; S09492; S68220; A33401; A53884; A60025; A27000

R;Binz, T.; Kurazono, H.; Wille, M.; Frevert, J.; Wernars, K.; Niemann, H.

J. Biol. Chem. 265, 9153-9158, 1990

A;Title: The complete sequence of botulinum neurotoxin type A and comparison with other clostridial neurotoxins.

A;Reference number: A35294; MUID:90264400; PMID:2160960

A;Accession: A35294

A;Molecule type: DNA

A;Residues: 1-1296 <BIN>

A;Cross-references: GB:M30196; NID:q144864; PIDN:AAA23262.1; PID:q144865

A;Experimental source: strain 62A, subtype A

R;Thompson, D.E.; Brehm, J.K.; Oultram, J.D.; Swinfield, T.J.; Shone, C.C.;

Atkinson, T.; Melling, J.; Minton, N.P.

Eur. J. Biochem. 189, 73-81, 1990

A;Title: The complete amino acid sequence of the Clostridium botulinum type A neurotoxin, deduced by nucleotide sequence analysis of the encoding gene.

A;Reference number: S09492; MUID:90235864; PMID:2185020

A;Accession: S09492

A;Molecule type: DNA

A;Residues: 1,'Q',3-26,'V',28-1296 <THO>

A;Cross-references: EMBL:X52066; NID:g40381; PIDN:CAA36289.1; PID:g40382

A;Experimental source: NCTC 2916

R; Fujita, R.; Fujinaga, Y.; Inoue, K.; Nakajima, H.; Kumon, H.; Oguma, K.

FEBS Lett. 376, 41-44, 1995

A;Title: Molecular characterization of two forms of nontoxic-nonhemagglutinin components of *Clostridium botulinum* type A progenitor toxins.

A;Reference number: S67988; MUID:96096783; PMID:8521962

A;Accession: S68220

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-12 <FUJ>

A;Cross-references: EMBL:D67030; DDBJ:D50421; NID:q2160224

R;Betley, M.J.; Somers, E.; DasGupta, B.R.

Biochem. Biophys. Res. Commun. 162, 1388-1395, 1989

A;Title: Characterization of botulinum' type A neurotoxin gene: delineation of the N-terminal encoding region.

A;Reference number: A33401; MUID:89350959; PMID:2669749

A;Accession: A33401

A;Molecule type: DNA

A;Residues: 1-35 <BET>

A;Cross-references: GB:M27892; NID:g144880; PIDN:AAA23269.1; PID:g551776
R;Gimenez, J.A.; DasGupta, B.R.
J. Protein Chem. 12, 351-363, 1993
A;Title: Botulinum type A neurotoxin digested with pepsin yields 132, 97, 72, 45, 42, and 18 kD fragments.
A;Reference number: A53884; MUID:94000342; PMID:8397793
A;Accession: A53884
A;Status: preliminary
A;Molecule type: protein
A;Residues: 867-880;1148-1217,'Y',1219 <GIM>
A;Experimental source: strain Hall
A;Note: sequence extracted from NCBI backbone (NCBIP:139159); sequence modified after extraction from NCBI backbone
R;DasGupta, B.R.; Dekleva, M.L.
Biochimie 72, 661-664, 1990
A;Title: Botulinum neurotoxin type A: sequence of amino acids at the N-terminus and around the nicking site.
A;Reference number: A60025; MUID:91120847; PMID:2126206
A;Accession: A60025
A;Molecule type: protein
A;Residues: 2-6;445-453,'X',455-457 <DAS1>
R;DasGupta, B.R.; Foley, J.; Niece, R.
Biochemistry 26, 4162, 1987
A;Title: Partial sequence of the light chain of botulinum neurotoxin type A.
A;Reference number: A27000
A;Accession: A27000
A;Molecule type: protein
A;Residues: 2-47 <DAS2>
R;Binz, T.; Blasi, J.; Yamasaki, S.; Baumeister, A.; Link, E.; Suedhof, T.C.; Jahn, R.; Niemann, H.
J. Biol. Chem. 269, 1617-1620, 1994
A;Title: Proteolysis of SNAP-25 by types E and A botulinal neurotoxins.
A;Reference number: A49708; MUID:94124495; PMID:8294407
A;Contents: annotation
C;Comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic synapses. This toxin is activated by cleavage into two chains linked by a disulfide bond.
C;Genetics:
A;Gene: atx; botA
C;Function:
A;Description: catalyzes hydrolysis of an Asn-Arg peptide bond in synaptosomal-associated 25K protein (SNAP-25)
C;Superfamily: tetanus toxin
C;Keywords: disulfide bond; hydrolase; metalloproteinase; neurotoxin; transmembrane protein; zinc
F;2-444/Product: bontoxilysin A light chain #status experimental <LGHT>
F;445-1296/Product: bontoxilysin A heavy chain #status experimental <HVY>
F;223,227/Binding site: zinc (His) #status predicted
F;224/Active site: Glu #status predicted

Query Match 52.7%; Score 59; DB 1; Length 1296;
Best Local Similarity 57.1%; Pred. No. 0.24;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FNNFTVSEFWLRVPK 14
: ||: |||:|:|
Db 938 YENFSTSEFWIRIPK 951

RESULT 8

A48940

bontoxilysin (EC 3.4.24.69) B precursor - Clostridium botulinum

N;Alternate names: botulinum neurotoxin type B (BoNT/B)

C;Species: Clostridium botulinum

C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999

C;Accession: A48940; S48105; S21575; A42871; S07155; S08562; S07128; S08573; S08574

R;Whelan, S.M.; Elmore, M.J.; Bodsworth, N.J.; Brehm, J.K.; Atkinson, T.; Minton, N.P.

Appl. Environ. Microbiol. 58, 2345-2354, 1992

A;Title: Molecular cloning of the Clostridium botulinum structural gene encoding the type B neurotoxin and determination of its entire nucleotide sequence.

A;Reference number: A48940; MUID:92384550; PMID:1514783

A;Accession: A48940

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1291 <WHE>

A;Cross-references: GB:M81186; NID:g144734; PIDN:AAA23211.1; PID:g144735

A;Experimental source: type B, Danish

A;Note: sequence extracted from NCBI backbone (NCBIN:112080, NCBIP:112081); this publication is not cited in GenBank entry CLOBOTB, release 103

R;Campbell, K.D.; Collins, M.D.; East, A.K.

J. Clin. Microbiol. 31, 2255-2262, 1993

A;Title: Gene probes for identification of the botulin neurotoxin gene and specific identification of neurotoxin types B, E, and F.

A;Reference number: S48103; MUID:94013372; PMID:8408542

A;Accession: S48105

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 634-994 <CAM>

A;Cross-references: EMBL:X70817; NID:g407782; PIDN:CAA50148.1; PID:g407783

A;Experimental source: proteolytic type B, strain NCTC 7273

R;Szabo, E.A.; Pemberton, J.M.; Desmarchelier, P.M.

submitted to the EMBL Data Library, April 1992

A;Description: Partial amino acid sequence of botulinum neurotoxin type B and comparison to other Clostridial neurotoxins.

A;Reference number: S21575

A;Accession: S21575

A;Molecule type: DNA

A;Residues: 36-217,'G',219-224,'S',226-246 <SZA>

A;Cross-references: EMBL:Z11934; NID:g40383; PIDN:CAA77991.1; PID:g40384

R;Kurazono, H.; Mochida, S.; Binz, T.; Eisel, U.; Quanz, M.; Grebenstein, O.; Wernars, K.; Poulain, B.; Tauc, L.; Niemann, H.

J. Biol. Chem. 267, 14721-14729, 1992

A;Title: Minimal essential domains specifying toxicity of the light chains of tetanus toxin and botulinum neurotoxin type A.

A;Reference number: A42871; MUID:92340509; PMID:1634516

A;Accession: A42871

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-313,'S',315-451 <KUR>

A;Experimental source: strain Okra

A;Note: sequence extracted from NCBI backbone (NCBIP:109365)

R;DasGupta, B.R.; Datta, A.

Biochimie 70, 811-817, 1988

A;Title: Botulinum neurotoxin type B (strain 657): partial sequence and similarity with tetanus toxin.

A;Reference number: S07155; MUID:89000987; PMID:3139097

A;Accession: S07155

A;Molecule type: protein

A;Residues: 2-29, 'M', 31-45 <DAS>

A;Accession: S08562

A;Molecule type: protein

A;Residues: 442-463, 'R', 465-467 <DA2>

R;Schmidt, J.J.; Sathyamoorthy, V.; DasGupta, B.R.

Arch. Biochem. Biophys. 238, 544-548, 1985

A;Title: Partial amino acid sequences of botulinum neurotoxins types B and E.

A;Reference number: S07128; MUID:85197963; PMID:3888113

A;Accession: S07128

A;Status: preliminary

A;Molecule type: protein

A;Residues: 2-16 <SCH1>

A;Accession: S08573

A;Status: preliminary

A;Molecule type: protein

A;Residues: 2-17 <SCH2>

A;Accession: S08574

A;Status: preliminary

A;Molecule type: protein

A;Residues: 442-459 <SCH3>

R;Schiavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.;

DasGupta, B.R.; Montecucco, C.

Nature 359, 832-835, 1992

A;Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteolytic cleavage of synaptobrevin.

A;Reference number: S27125; MUID:93063293; PMID:1331807

A;Contents: annotation

C;Comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic synapses. This toxin is activated by cleavage into two chains linked by a disulfide bond.

C;Genetics:

A;Gene: bont/b

C;Function:

A;Description: catalyzes hydrolysis of a Gln-Phe peptide bond in synaptobrevin 2

C;Superfamily: tetanus toxin

C;Keywords: hydrolase; metalloproteinase; neurotoxin; transmembrane protein; zinc

F;2-441/Product: bontoxilysin B light chain #status experimental <LGHT>

F;442-1291/Product: bontoxilysin B heavy chain #status experimental <HVY>

F;230,234/Binding site: zinc (His) #status predicted

F;231/Active site: Glu #status predicted

Query Match 51.8%; Score 58; DB 1; Length 1291;

Best Local Similarity 64.3%; Pred. No. 0.34;

Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPK 14

| :|:||||:|:|

Db 923 FLDFSVSFWIRIPK 936

RESULT 9

I40631

non-proteolytic botulinum neurotoxin type B precursor - Clostridium botulinum

C;Species: Clostridium botulinum

C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 16-Jul-1999

C;Accession: I40631; S48103; S48104; S36015

R;Hutson, R.A.; Collins, M.D.; East, A.K.; Thompson, D.E.

Curr. Microbiol. 28, 101-110, 1994

A;Title: Nucleotide sequence of the gene coding for non-proteolytic Clostridium botulinum type B neurotoxin: comparison with other clostridial neurotoxins.

A;Reference number: I40631; MUID:94122659; PMID:7764370

A;Accession: I40631

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1291 <RES>

A;Cross-references: EMBL:X71343; NID:g296148; PIDN:CAA50482.1; PID:g296149

R;Campbell, K.D.; Collins, M.D.; East, A.K.

J. Clin. Microbiol. 31, 2255-2262, 1993

A;Title: Gene probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F.

A;Reference number: S48103; MUID:94013372; PMID:8408542

A;Accession: S48103

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 634-761, 'E', 763-841, 'M', 843, 'T', 845, 'N', 847-994 <CAM1>

A;Cross-references: EMBL:X70814; NID:g407778; PIDN:CAA50145.1; PID:g407779

A;Experimental source: non-proteolytic strain 2129B (Scott)

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993

A;Accession: S48104

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 634-843, 'T', 845, 'N', 847-994 <CAM2>

A;Cross-references: EMBL:X70819; NID:g407780; PIDN:CAA50150.1; PID:g407781

A;Experimental source: non-proteolytic strain Eklund 2B (Colworth 229)

C;Comment: Botulinum neurotoxin type B in these strains may possess a capable catalytic site but are nonetheless inactive.

C;Genetics:

A;Gene: bont/b

C;Superfamily: tetanus toxin

C;Keywords: metalloprotein; neurotoxin; transmembrane protein; zinc

F;2-441/Product: botulinum neurotoxin type B light chain #status predicted <LGHT>

F;442-1291/Product: botulinum neurotoxin type B heavy chain #status predicted <HVY>

F;230,234/Binding site: zinc (His) #status predicted

F;231/Active site: Glu #status predicted

Query Match 51.8%; Score 58; DB 2; Length 1291;

Best Local Similarity 64.3%; Pred. No. 0.34;

Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FNNFTVSEFWLRVPK 14

| :|:||||:|:|

Db 923 FLDFSVSEFWIRIPK 936

RESULT 10

S48106

neurotoxin type E - Clostridium botulinum (fragment)

C;Species: Clostridium botulinum

C;Date: 14-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999

C;Accession: S48106

R;Campbell, K.D.; Collins, M.D.; East, A.K.

J. Clin. Microbiol. 31, 2255-2262, 1993

A;Title: Gene probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F.

A;Reference number: S48103; MUID:94013372; PMID:8408542

A;Accession: S48106

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-367 <CAM>

A;Cross-references: EMBL:X70818; NID:g407784; PIDN:CAA50149.1; PID:g407785

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993

C;Superfamily: tetanus toxin

C;Keywords: neurotoxin

Query Match	50.0%;	Score 56;	DB 2;	Length 367;
Best Local Similarity	53.8%;	Pred. No. 0.19;		
Matches	7;	Conservative	5;	Mismatches 1; Indels 0; Gaps 0;

Qy	1 FNNFTVSFWLRVP 13
	: :: : :
Db	297 YKNFSISFWVRIP 309

RESULT 11

JH0256

botulinum neurotoxin type E precursor - Clostridium butyricum

C;Species: Clostridium butyricum

C;Date: 30-Jun-1992 #sequence_revision 15-May-1998 #text_change 16-Jul-1999

C;Accession: JH0256; S16145

R;Poulet, S.; Hauser, D.; Quanz, M.; Niemann, H.; Popoff, M.R.

Biochem. Biophys. Res. Commun. 183, 107-113, 1992

A;Title: Sequences of the botulinal neurotoxin E derived from Clostridium botulinum type E (strain Beluga) and Clostridium butyricum (strains ATCC 43181 and ATCC 43755).

A;Reference number: JH0256; MUID:92181428; PMID:1543481

A;Accession: JH0256

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-27, 'E', 29-1251 <POU>

A;Cross-references: EMBL:X62088; NID:g40379

A;Experimental source: strains ATCC 43181 and ATCC 43755

R;Fujii, N.; Kimura, K.; Yashiki, T.; Indoh, T.; Murakami, T.; Tsuzuki, K.; Yokosawa, N.; Oguma, K.

J. Gen. Microbiol. 137, 519-525, 1991

A;Title: Cloning of a DNA fragment encoding the 5'-terminus of the botulinum type E toxin gene from Clostridium butyricum strain BL6340.

A;Reference number: S16145; MUID:91237316; PMID:2033376

A;Accession: S16145

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-229,'M',231-252 <FUJ>
 A;Cross-references: EMBL:X53180; NID:g40407; PIDN:CAA37321.1; PID:g40408
 A;Experimental source: strain BL6340
 C;Comment: The clostridial neurotoxins are toxins that inhibit neurotransmitter release at synaptic junctions.
 C;Comment: The heavy chain mediates the binding of toxin to cell receptors while the light chain appears to enter target cells.
 C;Superfamily: tetanus toxin
 C;Keywords: neurotoxin
 F;2-422/Product: botulinum neurotoxin type E light chain #status predicted <LIG>
 F;423-1251/Product: botulinum neurotoxin type E heavy chain #status predicted <HEA>
 F;412-426/Disulfide bonds: #status predicted

Query Match 50.0%; Score 56; DB 2; Length 1251;
 Best Local Similarity 53.8%; Pred. No. 0.72;
 Matches 7; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVP 13
 : ||::|||:|:|
 Db 912 YKNFSISFWVRIP 924

RESULT 12

S21178

botulinum neurotoxin type E precursor - Clostridium botulinum

C;Species: Clostridium botulinum

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Oct-1999

C;Accession: S21178; S48107; JH0257; B35294; A60027; S18111

R;Whelan, S.M.; Elmore, M.J.; Bodsworth, N.J.; Atkinson, T.; Minton, N.P.
 Eur. J. Biochem. 204, 657-667, 1992

A;Title: The complete amino acid sequence of the Clostridium botulinum type-E neurotoxin, derived by nucleotide-sequence analysis of the encoding gene.

A;Reference number: S21178; MUID:92174922; PMID:1541280

A;Accession: S21178

A;Molecule type: DNA

A;Residues: 1-1252 <WHE>

A;Cross-references: EMBL:X62683; NID:g40397; PIDN:CAA44558.1; PID:g40398

R;Campbell, K.D.; Collins, M.D.; East, A.K.

J. Clin. Microbiol. 31, 2255-2262, 1993

A;Title: Gene probes for identification of the botulinal neurotoxin gene and specific identification of neurotoxin types B, E, and F.

A;Reference number: S48103; MUID:94013372; PMID:8408542

A;Accession: S48107

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 616-982 <CAM>

A;Cross-references: EMBL:X70815; NID:g407786; PIDN:CAA50146.1; PID:g407787

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993

R;Poulet, S.; Hauser, D.; Quanz, M.; Niemann, H.; Popoff, M.R.
 Biochem. Biophys. Res. Commun. 183, 107-113, 1992

A;Title: Sequences of the botulinal neurotoxin E derived from Clostridium botulinum type E (strain Beluga) and Clostridium butyricum (strains ATCC 43181 and ATCC 43755).

A;Reference number: JH0256; MUID:92181428; PMID:1543481

A;Accession: JH0257

A;Status: nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-176,'R',178-197,'C',199-339,'R',341-772,'I',774-962,'FE',965-966,'R',968-1195,1197-1252 <POU>
 A;Cross-references: EMBL:X62089; NID:g40393; PIDN:CAA43999.1; PID:g40394
 A;Experimental source: strain Beluga
 R;Binz, T.; Kurazono, H.; Wille, M.; Frevert, J.; Wernars, K.; Niemann, H. J. Biol. Chem. 265, 9153-9158, 1990
 A;Title: The complete sequence of botulinum neurotoxin type A and comparison with other clostridial neurotoxins.
 A;Reference number: A35294; MUID:90264400; PMID:2160960
 A;Accession: B35294
 A;Status: not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-176,'R',178-252 <BIN>
 A;Experimental source: strain Beluga
 R;Gimenez, J.A.; DasGupta, B.R. Biochimie 72, 213-217, 1990
 A;Title: Botulinum neurotoxin type E fragmented with endoproteinase Lys-C reveals the site trypsin nicks and homology with tetanus neurotoxin.
 A;Reference number: A60027; MUID:90344918; PMID:2116911
 A;Accession: A60027
 A;Molecule type: protein
 A;Residues: 420-427 <GIM>
 A;Experimental source: strain Beluga
 A;Note: this fragment was generated by proteolysis with Lys-C rather than with trypsin
 C;Comment: The clostridial neurotoxins are highly potent protein toxins that inhibit neurotransmitter release at various synapses.
 C;Comment: The heavy chain mediates the binding of toxin to cell receptors while the light chain appears to enter target cells.
 C;Superfamily: tetanus toxin
 C;Keywords: neurotoxin
 F;1-422/Product: botulinum neurotoxin type E light chain #status predicted <LCH>
 F;423-1252/Product: botulinum neurotoxin type E heavy chain #status predicted <HCH>
 F;412-426/Disulfide bonds: #status predicted

Query Match 50.0%; Score 56; DB 2; Length 1252;
 Best Local Similarity 53.8%; Pred. No. 0.72;
 Matches 7; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVP 13
 : ||::|||:|:|
 Db 912 YKNFSISFWVRIP 924

RESULT 13
 I40645
 botulinum neurotoxin type A - Clostridium botulinum
 C;Species: Clostridium botulinum
 C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 16-Jul-1999
 C;Accession: I40645
 R;Willems, A.; East, A.K.; Lawson, P.A.; Collins, M.D. Res. Microbiol. 144, 547-556, 1993

A;Title: Sequence of the gene coding for the neurotoxin of Clostridium botulinum type A associated with infant botulism: comparison with other clostridial neurotoxins.

A;Reference number: I40645; MUID:94143603; PMID:8310180

A;Accession: I40645

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1296 <RES>

A;Cross-references: EMBL:X73423; NID:g507070; PIDN:CAA51824.1; PID:g507071

C;Superfamily: tetanus toxin

C;Keywords: neurotoxin

Query Match 50.0%; Score 56; DB 2; Length 1296;
Best Local Similarity 50.0%; Pred. No. 0.75;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FNNFTVSEFWLRVPK 14
: ||: |||::||
Db 938 YENFSTSEFWIKIPK 951

RESULT 14

S23158

nucleocapsid protein - Impatiens necrotic spot virus

C;Species: Impatiens necrotic spot virus

C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 20-Sep-1999

C;Accession: S23158

R;de Haan, P.; de Avila, A.C.; Kormelink, R.; Westerbroek, A.; Gielen, J.J.L.; Peters, D.; Goldbach, R.

FEBS Lett. 306, 27-32, 1992

A;Title: The nucleotide sequence of the S RNA of Impatiens necrotic spot virus, a novel tospovirus.

A;Reference number: S23158; MUID:92331780; PMID:1385787

A;Accession: S23158

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-449 <HAA>

A;Cross-references: EMBL:X66972; NID:g60488; PIDN:CAA47382.1; PID:g60489

A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 1 in having 104-Val, and 318-Met

C;Superfamily: tomato spotted wilt virus nonstructural protein NS

C;Keywords: nucleocapsid

Query Match 46.4%; Score 52; DB 2; Length 449;
Best Local Similarity 45.0%; Pred. No. 1.1;
Matches 9; Conservative 5; Mismatches 4; Indels 2; Gaps 1;

Qy 2 NN--FTVSEFWLRVPKVSASH 19
|| | :| |:|:|: |:
Db 240 NNKPFKISLWMRIPKIMKSN 259

RESULT 15

MNVUWC

nonstructural protein NS - tomato spotted wilt virus (strain CPNH1)

C;Species: tomato spotted wilt virus

C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 16-Jun-2000

C;Accession: JQ0547
R;de Haan, P.; Wagemakers, L.; Peters, D.; Goldbach, R.
J. Gen. Virol. 71, 1001-1007, 1990
A;Title: The S RNA segment of tomato spotted wilt virus has an ambisense
character.
A;Reference number: JQ0547; MUID:90264829; PMID:1693160
A;Accession: JQ0547
A;Molecule type: genomic RNA
A;Residues: 1-464 <DEH>
A;Cross-references: DDBJ:D00645; NID:g222685; PIDN:BAA00540.1; PID:g222686
C;Genetics:
A;Gene: NS
A;Map position: segment S
C;Superfamily: tomato spotted wilt virus nonstructural protein NS
C;Keywords: glycoprotein; nonstructural protein
F;132,210,270,291,381/Binding site: carbohydrate (Asn) (covalent) #status
predicted

Query Match 46.4%; Score 52; DB 1; Length 464;
Best Local Similarity 64.3%; Pred. No. 1.2;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NNFTVSFWLRVPKV 15
::| :| |||||
Db 239 SHFKLSLWLRVPKV 252

Search completed: August 13, 2004, 09:16:32
Job time : 2.15385 secs

OM protein - protein search, using sw model

Run on: August 13, 2004, 09:15:49 ; Search time 3.94872 Seconds
(without alignments)
1669.522 Million cell updates/sec

Title: US-09-785-215-6
Perfect score: 112
Sequence: 1 FNNFTVSFWLRVPKVSASHLE 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1292805 seqs, 313927144 residues

Total number of hits satisfying chosen parameters: 1292805

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query				Description
No.	Score	Match	Length	DB	ID	

1	112	100.0	21	9	US-09-943-548-3	Sequence 3, Appli
2	112	100.0	21	9	US-09-848-834A-4	Sequence 4, Appli
3	112	100.0	21	9	US-09-785-215-6	Sequence 6, Appli
4	112	100.0	21	10	US-09-405-986-2	Sequence 2, Appli
5	112	100.0	21	12	US-10-668-400-2	Sequence 2, Appli
6	112	100.0	21	12	US-09-943-334-3	Sequence 3, Appli
7	112	100.0	21	14	US-10-204-362-6	Sequence 6, Appli
8	112	100.0	21	14	US-10-339-522-3	Sequence 3, Appli
9	112	100.0	21	14	US-10-223-711-8	Sequence 8, Appli
10	112	100.0	21	14	US-10-223-809A-6	Sequence 6, Appli
11	112	100.0	21	14	US-10-261-208-5	Sequence 5, Appli
12	112	100.0	21	14	US-10-295-074-5	Sequence 5, Appli
13	112	100.0	21	15	US-10-372-111-8	Sequence 8, Appli
14	112	100.0	21	16	US-10-664-801-35	Sequence 35, Appl
15	112	100.0	21	16	US-10-699-517-10	Sequence 10, Appl
16	112	100.0	21	16	US-10-441-779C-13	Sequence 13, Appl
17	112	100.0	22	16	US-10-699-517-17	Sequence 17, Appl
18	112	100.0	28	16	US-10-699-517-35	Sequence 35, Appl
19	112	100.0	31	16	US-10-441-779C-17	Sequence 17, Appl
20	112	100.0	31	16	US-10-441-779C-18	Sequence 18, Appl
21	112	100.0	31	16	US-10-441-779C-19	Sequence 19, Appl
22	112	100.0	34	9	US-09-848-834A-10	Sequence 10, Appl
23	112	100.0	37	9	US-09-848-834A-14	Sequence 14, Appl
24	112	100.0	37	16	US-10-699-517-19	Sequence 19, Appl
25	112	100.0	43	16	US-10-699-517-36	Sequence 36, Appl
26	112	100.0	44	16	US-10-699-517-51	Sequence 51, Appl
27	112	100.0	50	9	US-09-848-834A-18	Sequence 18, Appl
28	112	100.0	51	16	US-10-699-517-52	Sequence 52, Appl
29	112	100.0	77	16	US-10-699-517-30	Sequence 30, Appl
30	112	100.0	79	16	US-10-699-517-49	Sequence 49, Appl
31	112	100.0	106	16	US-10-699-517-29	Sequence 29, Appl
32	112	100.0	158	14	US-10-297-942-2	Sequence 2, Appli
33	112	100.0	158	14	US-10-297-942-10	Sequence 10, Appl
34	112	100.0	158	14	US-10-297-942-12	Sequence 12, Appl
35	112	100.0	158	14	US-10-297-942-18	Sequence 18, Appl
36	112	100.0	158	14	US-10-297-942-20	Sequence 20, Appl
37	112	100.0	173	16	US-10-664-801-20	Sequence 20, Appl
38	112	100.0	188	16	US-10-664-801-14	Sequence 14, Appl
39	112	100.0	194	14	US-10-295-074-46	Sequence 46, Appl
40	112	100.0	194	14	US-10-295-074-47	Sequence 47, Appl
41	112	100.0	195	16	US-10-441-779C-38	Sequence 38, Appl
42	112	100.0	213	16	US-10-441-779C-40	Sequence 40, Appl
43	112	100.0	285	14	US-10-295-074-9	Sequence 9, Appli
44	112	100.0	285	14	US-10-295-074-11	Sequence 11, Appl
45	112	100.0	287	14	US-10-295-074-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1

US-09-943-548-3

; Sequence 3, Application US/09943548

; Patent No. US20020042364A1

; GENERAL INFORMATION:

; APPLICANT: Rittershaus, Charles W.

```

; APPLICANT: Thomas, Lawrence J.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP)
ACTIVITY
; FILE REFERENCE: TCS-411.1P US-1; Tcs-411.1P US-2
; CURRENT APPLICATION NUMBER: US/09/943,548
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 08/432,483
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: PCT/US96/06147
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/945,289
; PRIOR FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: helper T cell epitope of tetanus toxin
US-09-943-548-3

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Query Match          100.0%; Score 112; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 FNNFTVSFWLRVPKVSASHLE 21
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Db      1 FNNFTVSFWLRVPKVSASHLE 21

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RESULT 2

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US-09-848-834A-4
; Sequence 4, Application US/09848834A
; Patent No. US20020076416A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Chimeric Peptide Immunogens
; FILE REFERENCE: 1102865-0047
; CURRENT APPLICATION NUMBER: US/09/848,834A
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/202,328
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Tetanus bacillus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(21)
; OTHER INFORMATION: Amino acid sequence 947-967 of Tetanus
; OTHER INFORMATION: Toxoid Precursor (Tentoxylisin)
US-09-848-834A-4

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Query Match          100.0%; Score 112; DB 9; Length 21;

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Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPKVSASHLE 21
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Db 1 FNNFTVSFWLRVPKVSASHLE 21

RESULT 3

US-09-785-215-6

; Sequence 6, Application US/09785215
; Publication No. US20020187157A1
; GENERAL INFORMATION:
; APPLICANT: JENSEN, Martin Roland et al.
; TITLE OF INVENTION: NOVEL METHOD FOR DOWN-REGULATION OF AMYLOID
; FILE REFERENCE: 3631-0107P
; CURRENT APPLICATION NUMBER: US/09/785,215
; CURRENT FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Clostridium tetani
US-09-785-215-6

Query Match 100.0%; Score 112; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPKVSASHLE 21
|||||
Db 1 FNNFTVSFWLRVPKVSASHLE 21

RESULT 4

US-09-405-986-2

; Sequence 2, Application US/09405986
; Publication No. US20030157115A1
; GENERAL INFORMATION:
; APPLICANT: BAY, Sylvie
; APPLICANT: CANTACUZENE, Daniele
; APPLICANT: LECLERC, Claude
; APPLICANT: LO-MAN, Richard
; TITLE OF INVENTION: MULTIPLE ANTIGEN GLYCOPEPTIDE CARBOHYDRATE, VACCINE
; TITLE OF INVENTION: COMPRISING THE SAME AND USE THEREOF
; FILE REFERENCE: 134I US 3565
; CURRENT APPLICATION NUMBER: US/09/405,986
; CURRENT FILING DATE: 1999-09-27
; EARLIER APPLICATION NUMBER: 60/041,726
; EARLIER FILING DATE: 1997-03-27
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Clostridium tetani

US-09-405-986-2

Query Match 100.0%; Score 112; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 FNNFTVSEFWLRVPKVSASHLE 21

RESULT 5

US-10-668-400-2

; Sequence 2, Application US/10668400
; Publication No. US20040058859A1
; GENERAL INFORMATION:
; APPLICANT: Bay, Sylvie
; APPLICANT: Cantacuzene, Daniele
; APPLICANT: Leclerc, Claude
; APPLICANT: Lo-Man, Richard
; TITLE OF INVENTION: MULTIPLE ANTIGEN GLYCOPEPTIDE CARBOHYDRATE,
; TITLE OF INVENTION: VACCINE COMPRISING THE SAME AND USE THEREOF
; FILE REFERENCE: 102.166A-1
; CURRENT APPLICATION NUMBER: US/10/668,400
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 09/049,847
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/041,726
; PRIOR FILING DATE: 1997-03-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Clostridium tetani
US-10-668-400-2

Query Match 100.0%; Score 112; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 FNNFTVSEFWLRVPKVSASHLE 21

RESULT 6

US-09-943-334-3

; Sequence 3, Application US/09943334
; Publication No. US20040087481A1
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; APPLICANT: Thomas, Lawrence J.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP)
ACTIVITY
; FILE REFERENCE: TCS-411.1P US-1; Tcs-411.1P US-2
; CURRENT APPLICATION NUMBER: US/09/943,334

; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 08/432,483
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: PCT/US96/06147
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/945,289
; PRIOR FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: helper T cell epitope of tetanus toxin
US-09-943-334-3

Query Match 100.0%; Score 112; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPKVSASHLE 21
| | | | | | | | | | | | | | | | | | | | |
Db 1 FNNFTVSFWLRVPKVSASHLE 21

RESULT 7

US-10-204-362-6

; Sequence 6, Application US/10204362
; Publication No. US20030086938A1
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; TITLE OF INVENTION: No. US20030086938A1el Method For Down-Regulation Of
Amyloid
; FILE REFERENCE: 3631-0120P
; CURRENT APPLICATION NUMBER: US/10/204,362
; CURRENT FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 6
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Clostridium tetani
US-10-204-362-6

Query Match 100.0%; Score 112; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPKVSASHLE 21
| | | | | | | | | | | | | | | | | | | | |
Db 1 FNNFTVSFWLRVPKVSASHLE 21

RESULT 8

US-10-339-522-3

; Sequence 3, Application US/10339522

```

; Publication No. US20030108559A1
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; APPLICANT: Thomas, Lawrence J.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP)
ACTIVITY
; FILE REFERENCE: TCS-411.1P US-3
; CURRENT APPLICATION NUMBER: US/10/339,522
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 08/432,483
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: PCT/US96/06147
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/945,289
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 09/943,334
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 09/943,548
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: helper T cell epitope of tetanus toxin
US-10-339-522-3

```

```

Query Match          100.0%; Score 112; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 FNNFTVSEFWLRVPKVSASHLE 21
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Db      1 FNNFTVSEFWLRVPKVSASHLE 21

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RESULT 9

US-10-223-711-8

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; Sequence 8, Application US/10223711
; Publication No. US20030113344A1
; GENERAL INFORMATION:
; APPLICANT: Bakaletz, Lauren O.
; APPLICANT: Kaumaya, Pravin T.P.
; TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides
; FILE REFERENCE: 18525/04058
; CURRENT APPLICATION NUMBER: US/10/223,711
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 09/148,711
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 08/460,502
; PRIOR FILING DATE: 1995-06-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 21

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; TYPE: PRT
; ORGANISM: Clostridium tetani
US-10-223-711-8

Query Match 100.0%; Score 112; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSEFWLRVPKVSASHLE 21
|||||
Db 1 FNNFTVSEFWLRVPKVSASHLE 21

RESULT 10

US-10-223-809A-6

; Sequence 6, Application US/10223809A
; Publication No. US20030157117A1
; GENERAL INFORMATION:
; APPLICANT: Pharmexa A/S
; APPLICANT: Rasmussen, Peter Birk et al.
; TITLE OF INVENTION: No. US20030157117A1 Method for Down-Regulation of Amyloid
; FILE REFERENCE: 674542-2008.
; CURRENT APPLICATION NUMBER: US/10/223,809A
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: US 60/337,543
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 60/373,027
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: DE 2001 01231
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: DE 2002 0058
; PRIOR FILING DATE: 2002-04-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Clostridium tetani
US-10-223-809A-6

Query Match 100.0%; Score 112; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSEFWLRVPKVSASHLE 21
|||||
Db 1 FNNFTVSEFWLRVPKVSASHLE 21

RESULT 11

US-10-261-208-5

; Sequence 5, Application US/10261208
; Publication No. US20030158388A1
; GENERAL INFORMATION:
; APPLICANT: Rimoldi, Donata; Jongeneel, Victor; Coulie,
; Pierre; Cerrottini, Jean-Charles; Carrel,

```

;           Stefan; Reed, Daryl
;   TITLE OF INVENTION: MAGE-10 ENCODING cDNA, The Tumor
;                       Rejection Antigen Precuros Mage-10,
;                       Antibodies Specific To The Molecule, and
;                       Uses Thereof
;   NUMBER OF SEQUENCES: 5
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Felte & Lynch
;       STREET: 805 Third Avenue
;       CITY: New York City
;       STATE: New York
;       COUNTRY: USA
;       ZIP: 10022
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
;       COMPUTER: IBM
;       OPERATING SYSTEM: PC-DOS
;       SOFTWARE: Wordperfect
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/10/261,208
;       FILING DATE: 30-Sep-2002
;       CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: US/09/589,717
;       FILING DATE: 08-Jun-2000
;       APPLICATION NUMBER: 09/089,595
;       FILING DATE: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;       NAME: Hanson, No. US20030158388Alman D.
;       REGISTRATION NUMBER: 30,946
;       REFERENCE/DOCKET NUMBER: LUD 5457
;   TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (212) 688-9200
;       TELEFAX: (212) 838-3884
;   INFORMATION FOR SEQ ID NO: 5:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 21
;           TYPE: amino acid
;           TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-261-208-5

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Query Match          100.0%;  Score 112;  DB 14;  Length 21;
Best Local Similarity 100.0%;  Pred. No. 1.1e-10;
Matches 21;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1 FNNFTVSFWLRVPKVSASHLE 21
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Db      1 FNNFTVSFWLRVPKVSASHLE 21

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RESULT 12

US-10-295-074-5

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; Sequence 5, Application US/10295074
; Publication No. US20030185845A1
; GENERAL INFORMATION:
; APPLICANT: Pharmexa A/S

```

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; TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
; FILE REFERENCE: P1013DK00
; CURRENT APPLICATION NUMBER: US/10/295,074
; CURRENT FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Tetanus toxoid P30 epitope
US-10-295-074-5
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Query Match          100.0%; Score 112; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 FNNFTVSFWLRVPKVSASHLE 21
        ||||||||||||||||
Db      1 FNNFTVSFWLRVPKVSASHLE 21
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RESULT 13

US-10-372-111-8

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; Sequence 8, Application US/10372111
; Publication No. US20040009169A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, Julie
; APPLICANT: Yednock, Ted A.
; TITLE OF INVENTION: Administration of Agents for the Treatment of
Inflammation
; FILE REFERENCE: 002010-798
; CURRENT APPLICATION NUMBER: US/10/372,111
; CURRENT FILING DATE: 2003-05-25
; PRIOR APPLICATION NUMBER: US 60/374,501
; PRIOR FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/360,134
; PRIOR FILING DATE: 2002-02-25
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Tetanus toxoid
US-10-372-111-8
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Query Match          100.0%; Score 112; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 FNNFTVSFWLRVPKVSASHLE 21
        ||||||||||||||||
Db      1 FNNFTVSFWLRVPKVSASHLE 21
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RESULT 14

US-10-664-801-35

; Sequence 35, Application US/10664801
; Publication No. US20040115199A1
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 22021 PC 1
; CURRENT APPLICATION NUMBER: US/10/664,801
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US/09/396,937
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Clostridium tetani
US-10-664-801-35

Query Match 100.0%; Score 112; DB 16; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPKVSASHLE 21
|||||
Db 1 FNNFTVSFWLRVPKVSASHLE 21

RESULT 15

US-10-699-517-10

; Sequence 10, Application US/10699517
; Publication No. US20040136993A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceuticals, Inc.
; APPLICANT: Regents of the University of California
; APPLICANT: Schenk, Dale B.
; APPLICANT: Masliah, Eliezer
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF SYNUCLEINOPATHIC DISEASE
; FILE REFERENCE: 015270-008920US
; CURRENT APPLICATION NUMBER: US/10/699,517
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/423,012
; PRIOR FILING DATE: 2002-11-01
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Clostridium tetani
US-10-699-517-10

Query Match 100.0%; Score 112; DB 16; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSEFWLRVPKVSASHLE 21
| | | | | | | | | | | | | | | | | | | | | |
Db 1 FNNFTVSEFWLRVPKVSASHLE 21

Search completed: August 13, 2004, 09:33:24
Job time : 3.94872 secs

OM protein - protein search, using sw model

Run on: August 13, 2004, 09:07:53 ; Search time 3.20513 Seconds
(without alignments)
2067.275 Million cell updates/sec

Title: US-09-785-215-6
Perfect score: 112
Sequence: 1 FNNFTVSFWLRVPKVSASHLE 21

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertibrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%			
Result		Query			
No.	Score	Match	Length	ID	Description

1	112	100.0	451	2	Q9LA13	Q9la13 clostridium
2	112	100.0	1310	2	Q93N27	Q93n27 clostridium
3	62	55.4	1268	2	Q45851	Q45851 clostridium
4	61	54.5	1278	2	Q57236	Q57236 clostridium
5	58	51.8	361	2	Q45848	Q45848 clostridium
6	58	51.8	361	2	Q45846	Q45846 clostridium
7	58	51.8	441	2	Q9X708	Q9x708 clostridium
8	58	51.8	1291	2	Q9ZAJ8	Q9zaj8 clostridium
9	58	51.8	1291	2	Q93G71	Q93g71 clostridium
10	58	51.8	1291	2	Q933K0	Q933k0 clostridium
11	58	51.8	1291	2	Q08077	Q08077 clostridium
12	58	51.8	1291	2	Q8GR96	Q8gr96 clostridium
13	56	50.0	367	2	Q45861	Q45861 clostridium
14	56	50.0	367	2	Q45862	Q45862 clostridium
15	56	50.0	1251	2	Q9K395	Q9k395 clostridium
16	56	50.0	1252	2	Q8KZM3	Q8kzm3 clostridium
17	56	50.0	1255	2	Q9FAR6	Q9far6 clostridium
18	55	49.1	1280	2	Q9ZAJ5	Q9zaj5 clostridium
19	52	46.4	466	12	Q8JXJ9	Q8jxj9 tomato spot
20	52	46.4	466	12	Q8JXK0	Q8jxk0 tomato spot
21	52	46.4	467	12	Q8JXK2	Q8jxk2 tomato spot
22	52	46.4	467	12	O37369	O37369 tomato spot
23	52	46.4	467	12	O37367	O37367 tomato spot
24	52	46.4	467	12	Q8JVL0	Q8jvl0 tomato spot
25	52	46.4	467	12	Q8JXK4	Q8jxk4 tomato spot
26	51	45.5	467	12	Q88900	Q88900 tospovirus.
27	51	45.5	1196	2	Q45916	Q45916 clostridium
28	51	45.5	1196	2	Q53550	Q53550 clostridium
29	51	45.5	1196	2	Q9LBR2	Q9lbr2 clostridium
30	51	45.5	1196	2	Q9LBS8	Q9lbs8 clostridium
31	51	45.5	1196	2	Q93HT4	Q93ht4 clostridium
32	51	45.5	1196	9	Q9ZX77	Q9zx77 clostridium
33	51	45.5	1196	9	Q38197	Q38197 clostridium
34	50	44.6	466	16	Q88ZV4	Q88zv4 lactobacill
35	50	44.6	503	10	Q948E8	Q948e8 oryza sativ
36	50	44.6	503	10	Q8H892	Q8h892 oryza sativ
37	49	43.8	262	10	Q8GZE7	Q8gze7 pyrocystis
38	49	43.8	276	5	Q9TZK5	Q9tzk5 caenorhabdi
39	48	42.9	504	10	Q9M1N3	Q9mln3 arabidopsis
40	48	42.9	1285	2	Q45967	Q45967 clostridium
41	48	42.9	1285	2	Q9LBR1	Q9lbr1 clostridium
42	48	42.9	1291	2	Q93HT3	Q93ht3 clostridium
43	47.5	42.4	1275	12	Q9QTG7	Q9qtg7 clostridium
44	47.5	42.4	1280	2	Q45849	Q45849 clostridium
45	47.5	42.4	1280	2	Q9LBS7	Q9lbs7 clostridium

ALIGNMENTS

RESULT 1

Q9LA13

ID	Q9LA13	PRELIMINARY;	PRT;	451 AA.
AC	Q9LA13;			
DT	01-OCT-2000 (TrEMBLrel. 15, Created)			
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			

DE Tetanus toxin (Fragment).
 OS Clostridium tetani.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=20886;
 RA He H.J., Shi H.J., He Z.Y., Yuan Q.S., Wu X.F.;
 RT "Fragment C of Tetanus Toxin."
 RL Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF154828; AAF73267.1; -.
 DR HSSP; P04958; 1A8D.
 DR GO; GO:0004866; F:endorpeptidase inhibitor activity; IEA.
 DR InterPro; IPR008985; ConA_like_lec_gl.
 DR InterPro; IPR001064; Crystallin.
 DR InterPro; IPR002160; Kunitz_legume.
 DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 451 AA; 51823 MW; 69A8C5F030E6CD8E CRC64;

Query Match 100.0%; Score 112; DB 2; Length 451;
 Best Local Similarity 100.0%; Pred. No. 3.8e-10;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPKVSASHLE 21
 |||||
 Db 83 FNNFTVSFWLRVPKVSASHLE 103

RESULT 2

Q93N27

ID Q93N27 PRELIMINARY; PRT; 1310 AA.
 AC Q93N27;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Tetanus toxin (Fragment).
 OS Clostridium tetani.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shumin Z., Dianliang L.;
 RT "Cloning and sequence analysis of tetanus toxin gene."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF389424; AAK72964.2; -.
 DR GO; GO:0004866; F:endorpeptidase inhibitor activity; IEA.
 DR GO; GO:0008237; F:metallopeptidase activity; IEA.
 DR GO; GO:0015070; F:toxin activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR008985; ConA_like_lec_gl.
 DR InterPro; IPR001064; Crystallin.
 DR InterPro; IPR002160; Kunitz_legume.

DR InterPro; IPR000395; Peptidase_M27.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR Pfam; PF01742; Peptidase_M27; 1.
 DR PRINTS; PR00760; BONTOLILYSIN.
 DR ProDom; PD001963; Bontolilysin; 1.
 DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 FT NON_TER 1 1
 FT NON_TER 1310 1310
 SQ SEQUENCE 1310 AA; 150316 MW; 9EADDC914418E450 CRC64;

Query Match 100.0%; Score 112; DB 2; Length 1310;
 Best Local Similarity 100.0%; Pred. No. 1.1e-09;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPKVSASHLE 21
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 Db 948 FNNFTVSFWLRVPKVSASHLE 968

RESULT 3

Q45851

ID Q45851 PRELIMINARY; PRT; 1268 AA.
 AC Q45851;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Neurotoxin type F.
 GN BONT /F.
 OS Clostridium baratii.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1561;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93252228; PubMed=8486245;
 RA Thompson D.E., Hutson R.A., East A.K., Allaway D., Collins M.D.,
 RA Richardson P.T.;
 RT "Nucleotide sequence of the gene coding for Clostridium barati type F
 RT neurotoxin: Comparison with other clostridial neurotoxins."
 RL FEMS Microbiol. Lett. 108:175-182(1993).
 DR EMBL; X68262; CAA48329.1; -.
 DR PIR; S33411; S33411.
 DR HSSP; P10845; 3BTA.
 DR MEROPS; M27.002; -.
 DR GO; GO:0004866; F:endopeptidase inhibitor activity; IEA.
 DR GO; GO:0008237; F:metallopeptidase activity; IEA.
 DR GO; GO:0015070; F:toxin activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR008985; ConA_like_lec_gl.
 DR InterPro; IPR002160; Kunitz_legume.
 DR InterPro; IPR000395; Peptidase_M27.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR Pfam; PF01742; Peptidase_M27; 1.
 DR PRINTS; PR00760; BONTOLILYSIN.

DR ProDom; PD001963; Bontoxilysin; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
SQ SEQUENCE 1268 AA; 145513 MW; 963040091AC15ED2 CRC64;

Query Match 55.4%; Score 62; DB 2; Length 1268;
Best Local Similarity 64.3%; Pred. No. 0.23;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPK 14
: ||:||||:|:|
Db 922 YQNFSVSFWVRIPK 935

RESULT 4

Q57236

ID Q57236 PRELIMINARY; PRT; 1278 AA.
AC Q57236; Q45863;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Botulinum neurotoxin type F (BONT/F protein).
GN BONT/F.
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 10281;
RA Hutson R.A., Collins M.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Elmore M.J., Bodsworth N.J., Whelan S.M., Minton N.P.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE OF 635-1000 FROM N.A.
RC STRAIN=NCTC 1028;
RX MEDLINE=94013372; PubMed=8408542;
RA Campbell K., East A.K., Collins M.D.;
RT "Gene probes for identification of the botulinal neurotoxin gene and
RT specific identification of neurotoxin types B, E, and F.";
RL J. Clin. Microbiol. 31:2255-2262(1993).
RN [4]
RP SEQUENCE OF 1-27 FROM N.A.
RC STRAIN=LANGELAND;
RX MEDLINE=98404102; PubMed=9732534;
RA East A.K., Bhandari M., Hielm S., Collins M.D.;
RT "Analysis of the botulinum neurotoxin type F gene clusters in
RT proteolytic and nonproteolytic Clostridium botulinum and Clostridium
RT barati.";
RL Curr. Microbiol. 37:262-268(1998).
DR EMBL; X81714; CAA57358.1; -.
DR EMBL; L35496; AAA23210.1; -.
DR EMBL; X70821; CAA50152.1; -.
DR EMBL; X99064; CAA67512.1; -.
DR PIR; S48110; S48110.

DR HSSP; P10845; 3BTA.
 DR MEROPS; M27.002; -.
 DR GO; GO:0004866; F:endopeptidase inhibitor activity; IEA.
 DR GO; GO:0008237; F:metallopeptidase activity; IEA.
 DR GO; GO:0015070; F:toxin activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR008985; ConA_like_lec_gl.
 DR InterPro; IPR002160; Kunitz_legume.
 DR InterPro; IPR000395; Peptidase_M27.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR Pfam; PF01742; Peptidase_M27; 1.
 DR PRINTS; PR00760; BONTOXILYSIN.
 DR ProDom; PD001963; Bontoxilysin; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KW Neurotoxin.
 SQ SEQUENCE 1278 AA; 147073 MW; A1BE1318431D6918 CRC64;

Query Match 54.5%; Score 61; DB 2; Length 1278;
 Best Local Similarity 57.1%; Pred. No. 0.34;
 Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPK 14
 : ||::|||:|:|
 Db 931 YQNFSISFWVRIPK 944

RESULT 5

Q45848

ID Q45848 PRELIMINARY; PRT; 361 AA.
 AC Q45848;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Botulinum neurotoxin type B (Fragment).
 GN BONT/B.
 OS Clostridium botulinum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=type B;
 RX MEDLINE=94013372; PubMed=8408542;
 RA Campbell K., East A.K., Collins M.D.;
 RT "Gene probes for identification of the botulinal neurotoxin gene and
 RT specific identification of neurotoxin types B, E, and F."
 RL J. Clin. Microbiol. 31:2255-2262(1993).
 DR EMBL; X70819; CAA50150.1; -.
 DR HSSP; P10845; 3BTA.
 DR GO; GO:0015070; F:toxin activity; IEA.
 DR InterPro; IPR008985; ConA_like_lec_gl.
 KW Neurotoxin.
 FT NON_TER 1 1
 FT NON_TER 361 361
 SQ SEQUENCE 361 AA; 42131 MW; A2E0FFFC81F9533D CRC64;

Query Match 51.8%; Score 58; DB 2; Length 361;
Best Local Similarity 64.3%; Pred. No. 0.29;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FNNFTVSEFWLRVPK 14
| :|:||||:|:|
Db 290 FLDFSVSEFWIRIPK 303

RESULT 6

Q45846

ID Q45846 PRELIMINARY; PRT; 361 AA.
AC Q45846;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Botulinum neurotoxin type B (Fragment).
GN BONT/B.
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=type B;
RX MEDLINE=94013372; PubMed=8408542;
RA Campbell K., East A.K., Collins M.D.;
RT "Gene probes for identification of the botulinal neurotoxin gene and
RT specific identification of neurotoxin types B, E, and F.";
RL J. Clin. Microbiol. 31:2255-2262(1993).
DR EMBL; X70814; CAA50145.1; -.
DR HSSP; P10845; 3BTA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR InterPro; IPR008985; ConA_like_lec_gl.
KW Neurotoxin.
FT NON_TER 1 1
FT NON_TER 361 361
SQ SEQUENCE 361 AA; 42175 MW; 533EA98735CD98E1 CRC64;

Query Match 51.8%; Score 58; DB 2; Length 361;
Best Local Similarity 64.3%; Pred. No. 0.29;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FNNFTVSEFWLRVPK 14
| :|:||||:|:|
Db 290 FLDFSVSEFWIRIPK 303

RESULT 7

Q9X708

ID Q9X708 PRELIMINARY; PRT; 441 AA.
AC Q9X708;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Botulinum neurotoxin type B (Fragment).

GN BONT/B.
 OS Clostridium botulinum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99343691; PubMed=10413679;
 RA Lalli G., Herreros J., Osborne S.L., Montecucco C., Rossetto O.,
 RA Schiavo G.;
 RT "Functional characterisation of tetanus and botulinum neurotoxins
 RT binding domains.";
 RL J. Cell Sci. 112:2715-2724(1999).
 DR EMBL; AJ242628; CAB43706.1; -.
 DR HSSP; P10845; 3BTA.
 DR GO; GO:0004866; F:endopeptidase inhibitor activity; IEA.
 DR GO; GO:0015070; F:toxin activity; IEA.
 DR InterPro; IPR008985; ConA_like_lec_gl.
 DR InterPro; IPR002160; Kunitz_legume.
 KW Neurotoxin.
 FT NON_TER 1 1
 FT NON_TER 441 441
 SQ SEQUENCE 441 AA; 52772 MW; 721D0B468E8C95A4 CRC64;

Query Match 51.8%; Score 58; DB 2; Length 441;
 Best Local Similarity 64.3%; Pred. No. 0.36;
 Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FNNFTVSEFWLRVVK 14
 | :|:||||:|:|
 Db 81 FLDFSVSEFWIRIPK 94

RESULT 8

Q9ZAJ8

ID Q9ZAJ8 PRELIMINARY; PRT; 1291 AA.
 AC Q9ZAJ8;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE BonT protein.
 GN BONT.
 OS Clostridium botulinum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 3281;
 RX MEDLINE=98440323; PubMed=9767710;
 RA Santos-Buelga J., Collins M.D., East A.K.;
 RT "Characterization of the genes encoding the Botulinum neurotoxin
 RT complex in a strain of clostridium botulinum producing type B & F
 RT neurotoxins.";
 RL Curr. Microbiol. 37:312-318(1998).
 DR EMBL; Y13630; CAA73968.1; -.
 DR HSSP; P10845; 3BTA.

DR GO; GO:0004866; F:endorpeptidase inhibitor activity; IEA.
 DR GO; GO:0008237; F:metallopeptidase activity; IEA.
 DR GO; GO:0015070; F:toxin activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR008985; ConA_like_lec_gl.
 DR InterPro; IPR002160; Kunitz_legume.
 DR InterPro; IPR000395; Peptidase_M27.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR Pfam; PF01742; Peptidase_M27; 1.
 DR PRINTS; PR00760; BONTOLILYSIN.
 DR ProDom; PD001963; Bontolilysin; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 SQ SEQUENCE 1291 AA; 150840 MW; E4D3B0E46AB2E735 CRC64;

Query Match 51.8%; Score 58; DB 2; Length 1291;
 Best Local Similarity 64.3%; Pred. No. 1.1;
 Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPK 14
 | :|:||||:|:|
 Db 923 FLDFSVSFWIRIPK 936

RESULT 9

Q93G71

ID Q93G71 PRELIMINARY; PRT; 1291 AA.
 AC Q93G71;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Neurotoxin type B.
 OS Clostridium botulinum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1436;
 RA Kirma N., Ferreira J.L., Baumstark B.R.;
 RT "Characterization of six type A strains of Clostridium botulinum that
 RT contain type B toxin gene sequences."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF295926; AAK97132.1; -.
 DR GO; GO:0004866; F:endorpeptidase inhibitor activity; IEA.
 DR GO; GO:0008237; F:metallopeptidase activity; IEA.
 DR GO; GO:0015070; F:toxin activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR008985; ConA_like_lec_gl.
 DR InterPro; IPR002160; Kunitz_legume.
 DR InterPro; IPR000395; Peptidase_M27.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR Pfam; PF01742; Peptidase_M27; 1.
 DR PRINTS; PR00760; BONTOLILYSIN.

DR ProDom; PD001963; Bontoxilysin; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
SQ SEQUENCE 1291 AA; 150824 MW; D7CA07BAE2EB8CD2 CRC64;

Query Match 51.8%; Score 58; DB 2; Length 1291;
Best Local Similarity 64.3%; Pred. No. 1.1;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPK 14
| :|:|||||:|:|
Db 923 FLDFSVSFWIRIPK 936

RESULT 10

Q933K0

ID Q933K0 PRELIMINARY; PRT; 1291 AA.
AC Q933K0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Type B cryptic neurotoxin.
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=593, and 588;
RA Kirma N., Ferreira J.L., Baumstark B.R.;
RT "Characterization of six type A strains of Clostridium botulinum that
RT contain type B toxin gene sequences."
RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF300466; AAL11499.1; -.
DR EMBL; AF300465; AAL11498.1; -.
DR GO; GO:0004866; F:endopeptidase inhibitor activity; IEA.
DR GO; GO:0008237; F:metallopeptidase activity; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR008985; ConA_like_lec_gl.
DR InterPro; IPR002160; Kunitz_legume.
DR InterPro; IPR000395; Peptidase_M27.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF01742; Peptidase_M27; 1.
DR PRINTS; PR00760; BONTOXILYSIN.
DR ProDom; PD001963; Bontoxilysin; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Neurotoxin.
SQ SEQUENCE 1291 AA; 150843 MW; 7AC1737B0FA5A151 CRC64;

Query Match 51.8%; Score 58; DB 2; Length 1291;
Best Local Similarity 64.3%; Pred. No. 1.1;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPK 14
| :|:|||||:|:|

Db 923 FLDFSVSEFWIRIPK 936

RESULT 11

Q08077

ID Q08077 PRELIMINARY; PRT; 1291 AA.
AC Q08077;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE BoNT/B.
GN BONT/B.
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Eklund 17B ATCC25765;
RX MEDLINE=94122659; PubMed=7764370;
RA Hutson R.A., Collins M.D., East A.K., Thompson D.E.;
RT "Nucleotide sequence of the gene coding for non-proteolytic
RT Clostridium botulinum type B neurotoxin: comparison with other
RT clostridial neurotoxins."
RL Curr. Microbiol. 28:101-110(1994).
DR EMBL; X71343; CAA50482.1; -.
DR PIR; I40631; I40631.
DR HSSP; P10845; 3BTA.
DR MEROPS; M27.002; -.
DR GO; GO:0004866; F:endopeptidase inhibitor activity; IEA.
DR GO; GO:0008237; F:metallopeptidase activity; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR008985; ConA_like_lec_gl.
DR InterPro; IPR002160; Kunitz_legume.
DR InterPro; IPR000395; Peptidase_M27.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF01742; Peptidase_M27; 1.
DR PRINTS; PR00760; BONTXILYSIN.
DR ProDom; PD001963; Bontoxilysin; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
SQ SEQUENCE 1291 AA; 150513 MW; 71BCAFE23D69FAAA CRC64;

Query Match 51.8%; Score 58; DB 2; Length 1291;
Best Local Similarity 64.3%; Pred. No. 1.1;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FNNFTVSEFWLRVPK 14
| :|:|||||:|:|
Db 923 FLDFSVSEFWIRIPK 936

RESULT 12

Q8GR96

ID Q8GR96 PRELIMINARY; PRT; 1291 AA.

AC Q8GR96;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Neurotoxin.
 GN BONTB.
 OS Clostridium botulinum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ihara H., Kohda T., Morimoto F., Tsukamoto K., Karasawa T.,
 RA Nakamura S., Mukamoto M., Kozaki S.;
 RT "Clostridium botulinum type B neurotoxin associated with infant
 RT botulism.";
 RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB084152; BAC22064.1; -.
 DR GO; GO:0004866; F:endopeptidase inhibitor activity; IEA.
 DR GO; GO:0008237; F:metallopeptidase activity; IEA.
 DR GO; GO:0015070; F:toxin activity; IEA.
 DR GO; GO:0008270; F:zinc ion binding; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR008985; ConA_like_lec_gl.
 DR InterPro; IPR002160; Kunitz_legume.
 DR InterPro; IPR000395; Peptidase_M27.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR Pfam; PF01742; Peptidase_M27; 1.
 DR PRINTS; PR00760; BONTOXILYSIN.
 DR ProDom; PD001963; Bontoxilysin; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 SQ SEQUENCE 1291 AA; 150574 MW; 0227CAEF4F58504D CRC64;

Query Match 51.8%; Score 58; DB 2; Length 1291;
 Best Local Similarity 64.3%; Pred. No. 1.1;
 Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FNNFTVSEFWLRVVK 14
 | :|:||||:|:|
 Db 923 FLDFSVSEFWIRIPK 936

RESULT 13

Q45861

ID Q45861 PRELIMINARY; PRT; 367 AA.
 AC Q45861;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Botulinum neurotoxin type E (Fragment).
 GN BONT/E.
 OS Clostridium botulinum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1491;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=type E;
 RX MEDLINE=94013372; PubMed=8408542;
 RA Campbell K., East A.K., Collins M.D.;
 RT "Gene probes for identification of the botulinal neurotoxin gene and
 RT specific identification of neurotoxin types B, E, and F.";
 RL J. Clin. Microbiol. 31:2255-2262(1993).
 DR EMBL; X70818; CAA50149.1; -.
 DR PIR; S48106; S48106.
 DR HSSP; P10845; 3BTA.
 DR GO; GO:0015070; F:toxin activity; IEA.
 DR InterPro; IPR008985; ConA_like_lec_gl.
 KW Neurotoxin.
 FT NON_TER 1 1
 FT NON_TER 367 367
 SQ SEQUENCE 367 AA; 42902 MW; 346A610C2FF70262 CRC64;

Query Match 50.0%; Score 56; DB 2; Length 367;
 Best Local Similarity 53.8%; Pred. No. 0.64;
 Matches 7; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVP 13
 : ||::|||:|:|
 Db 297 YKNFSISFWVRIP 309

RESULT 14

Q45862

ID Q45862 PRELIMINARY; PRT; 367 AA.
 AC Q45862;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Botulinum neurotoxin type E (Fragment).
 GN BONT/E.
 OS Clostridium botulinum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=type E;
 RX MEDLINE=94013372; PubMed=8408542;
 RA Campbell K., East A.K., Collins M.D.;
 RT "Gene probes for identification of the botulinal neurotoxin gene and
 RT specific identification of neurotoxin types B, E, and F.";
 RL J. Clin. Microbiol. 31:2255-2262(1993).
 DR EMBL; X70815; CAA50146.1; -.
 DR PIR; S21178; S21178.
 DR HSSP; P10845; 3BTA.
 DR GO; GO:0015070; F:toxin activity; IEA.
 DR InterPro; IPR008985; ConA_like_lec_gl.
 KW Neurotoxin.
 FT NON_TER 1 1
 FT NON_TER 367 367
 SQ SEQUENCE 367 AA; 42854 MW; 0810595B3A865570 CRC64;

Query Match 50.0%; Score 56; DB 2; Length 367;
Best Local Similarity 53.8%; Pred. No. 0.64;
Matches 7; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 FNNFTVSEFWLRVP 13
: ||::|||:|:|
Db 297 YKNFSISFWVRIP 309

RESULT 15

Q9K395

ID Q9K395 PRELIMINARY; PRT; 1251 AA.
AC Q9K395;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Type E botulinum toxin.
GN BONT/E.
OS Clostridium butyricum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1492;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LCL 095;
RA Wang X., Maegawa T., Kozaki S., Tsukamoto K., Kato H., Nakamura S.,
RA Karasawa T.;
RT "C. butyricum (LCL 095) gene for type E botulinum toxin.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LCL 155;
RA Wang X., Maegawa T., Kozaki S., Tsukamoto K., Gyobu Y., Yamakawa K.,
RA Kato H., Nakamura S., Karasawa T.;
RT "C. butyricum (LCL 155) gene for type E botulinum toxin.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=KZ 1899;
RA Wang X., Maegawa T., Kozaki S., Tsukamoto K., Kato H., Nakamura S.,
RA Karasawa T.;
RT "C. butyricum (KZ 1899) gene for type E botulinum toxin.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=KZ 1897;
RA Wang X., Maegawa T., Kozaki S., Tsukamoto K., Kato H., Nakamura S.,
RA Karasawa T.;
RT "C. butyricum (KZ 1897) gene for type E botulinum toxin.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=KZ 1898;
RA Wang X., Maegawa T., Kozaki S., Tsukamoto K., Kato H., Nakamura S.,
RA Karasawa T.;
RT "C. butyricum (KZ 1898) gene for type E botulinum toxin.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KZ 1886;
 RA Wang X., Maegawa T., Kozaki S., Tsukamoto K., Kato H., Nakamura S.,
 RA Karasawa T.;
 RT "C. butyricum (KZ 1886) gene for type E botulinum toxin.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KZ 1887;
 RA Wang X., Maegawa T., Kozaki S., Tsukamoto K., Kato H., Nakamura S.,
 RA Karasawa T.;
 RT "C. butyricum (KZ 1887) gene for type E botulinum toxin.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KZ 1889;
 RA Wang X., Maegawa T., Kozaki S., Tsukamoto K., Kato H., Nakamura S.,
 RA Karasawa T.;
 RT "C. butyricum (KZ 1889) gene for type E botulinum toxin.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KZ 1890;
 RA Wang X., Maegawa T., Kozaki S., Tsukamoto K., Kato H., Nakamura S.,
 RA Karasawa T.;
 RT "C. butyricum (KZ 1890) gene for type E botulinum toxin.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
 RN [10]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KZ 1891;
 RA Wang X., Maegawa T., Kozaki S., Tsukamoto K., Kato H., Nakamura S.,
 RA Karasawa T.;
 RT "C. butyricum (KZ 1891) gene for type E botulinum toxin.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
 RN [11]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LCL 063;
 RA Wang X., Maegawa T., Kozaki S., Tsukamoto K., Kato H., Nakamura S.,
 RA Karasawa T.;
 RT "C. butyricum (LCL 063) gene for type E botulinum toxin.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AB037714; BAB03522.1; -.
 DR EMBL; AB037704; BAB03512.1; -.
 DR EMBL; AB037705; BAB03513.1; -.
 DR EMBL; AB037706; BAB03514.1; -.
 DR EMBL; AB037707; BAB03515.1; -.
 DR EMBL; AB037708; BAB03516.1; -.
 DR EMBL; AB037709; BAB03517.1; -.
 DR EMBL; AB037710; BAB03518.1; -.
 DR EMBL; AB037711; BAB03519.1; -.
 DR EMBL; AB037712; BAB03520.1; -.
 DR EMBL; AB037713; BAB03521.1; -.
 DR HSSP; P10845; 3BTA.
 DR GO; GO:0004866; F:endopeptidase inhibitor activity; IEA.
 DR GO; GO:0008237; F:metallopeptidase activity; IEA.
 DR GO; GO:0015070; F:toxin activity; IEA.

DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR008985; ConA_like_lectin.
DR InterPro; IPR002160; Kunitz_legume.
DR InterPro; IPR000395; Peptidase_M27.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF01742; Peptidase_M27; 1.
DR PRINTS; PR00760; BONTOXILYSIN.
DR ProDom; PD001963; Bontoxilysin; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
SQ SEQUENCE 1251 AA; 143751 MW; 2021F4E427070296 CRC64;

Query Match 50.0%; Score 56; DB 2; Length 1251;
Best Local Similarity 53.8%; Pred. No. 2.3;
Matches 7; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FNNFTVSEFWLRVP 13
: ||::|||:|:|
Db 912 YKNFSISFWVRIP 924

Search completed: August 13, 2004, 09:15:39
Job time : 6.20513 secs

OM protein - protein search, using sw model

Run on: August 13, 2004, 09:07:28 ; Search time 0.769231 Seconds
 (without alignments)
 1421.515 Million cell updates/sec

Title: US-09-785-215-6
 Perfect score: 112
 Sequence: 1 FNNFTVSEFWLRVPKVSASHLE 21

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match	Length				
1	112	100.0	1314	1	TETX_CLOTE	P04958	clostridium
2	61	54.5	1274	1	BXF_CLOBO	P30996	clostridium
3	61	54.5	1296	1	BXG_CLOBO	Q60393	clostridium
4	59	52.7	1295	1	BXA1_CLOBO	P10845	clostridium
5	58	51.8	1290	1	BXB_CLOBO	P10844	clostridium
6	57	50.9	1051	1	VP2_AHSV6	O71024	african hor
7	56	50.0	1250	1	BXE_CLOBO	Q00496	clostridium
8	56	50.0	1250	1	BXE_CLOBU	P30995	clostridium
9	56	50.0	1295	1	BXA2_CLOBO	Q45894	clostridium
10	52	46.4	449	1	VNSS_INSVN	Q01811	impatiens n
11	52	46.4	464	1	VNSS_TSWV1	P26002	tomato spot
12	52	46.4	467	1	VNSS_TSWVL	P26003	tomato spot
13	51	45.5	1196	1	BXCN_CLOBO	P46081	clostridium
14	48	42.9	1290	1	BXC1_CLOBO	P18640	clostridium
15	47.5	42.4	1276	1	BXD_CLOBO	P19321	clostridium
16	47	42.0	760	1	AMY_CLOAB	P23671	clostridium
17	46	41.1	1162	1	BXEN_CLOBO	P46082	clostridium

18	46	41.1	1162	1	BXEN_CLOBU	Q06366	clostridium
19	45	40.2	639	1	CGMA_RHIME	P72302	rhizobium m
20	44	39.3	241	1	CRTA_RHOCA	P17055	rhodobacter
21	43	38.4	152	1	YOBD_ECO57	Q8xcp5	escherichia
22	43	38.4	152	1	YOBD_ECOLI	P76263	escherichia
23	43	38.4	867	1	RRPO_BYDVI	P29044	barley yell
24	42	37.5	158	1	YOBD_SHIFL	Q83178	shigella fl
25	42	37.5	208	1	FTSQ_STRGR	P45503	streptomyce
26	42	37.5	789	1	AI2M_YEAST	P03876	saccharomyc
27	42	37.5	1337	1	YDM5_SCHPO	P87136	schizosacch
28	42	37.5	1539	1	SMCY_HUMAN	Q9by66	homo sapien
29	42	37.5	1548	1	SMCY_MOUSE	Q62240	mus musculu
30	42	37.5	1554	1	SMCX_MOUSE	P41230	mus musculu
31	42	37.5	1560	1	SMCX_HUMAN	P41229	homo sapien
32	41.5	37.1	237	1	YBS0_YEAST	P38242	saccharomyc
33	41.5	37.1	559	1	OPGG_PSEPK	Q88d03	pseudomonas
34	41.5	37.1	728	1	YJ89_YEAST	P47156	saccharomyc
35	41	36.6	352	1	CITC_ECOLI	P77390	escherichia
36	41	36.6	3584	1	NBEA_DROME	Q9w4e2	drosophila
37	40.5	36.2	230	1	FIMC_SALTY	P37923	salmonella
38	40.5	36.2	535	1	YA98_SCHPO	Q09786	schizosacch
39	40	35.7	116	1	NU3M_PAROL	P92817	paralichthy
40	40	35.7	118	1	YMX2_YEAST	Q04276	saccharomyc
41	40	35.7	269	1	PARA_MYCGE	P47706	mycoplasma
42	40	35.7	288	1	PEF1_SCHPO	O74456	schizosacch
43	40	35.7	385	1	G22C_DROME	P58952	drosophila
44	40	35.7	390	1	DACD_SALTY	P37604	salmonella
45	40	35.7	396	1	YJE8_YEAST	P47049	saccharomyc

ALIGNMENTS

RESULT 1

TETX_CLOTE

ID TETX_CLOTE STANDARD; PRT; 1314 AA.
 AC P04958;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tetanus toxin precursor (EC 3.4.24.68) (Tentoxylisin) [Contains:
 DE Tetanus toxin light chain (Tetanus toxin chain L); Tetanus toxin heavy
 DE chain (Tetanus toxin chain H)].
 GN TETX OR CTP60.
 OS Clostridium tetani.
 OG Plasmid pE88, and Plasmid 75 Kbp.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC PLASMID=75 Kbp;
 RX MEDLINE=87053814; PubMed=3536478;
 RA Eisel U., Jarausch W., Goretzki K., Henschen A., Engels J.,
 RA Weller U., Hudel M., Habermann E., Niemann H.;
 RT "Tetanus toxin: primary structure, expression in E. coli, and
 RT homology with botulinum toxins."

RL EMBO J. 5:2495-2502(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CN3911; PLASMID=75 Kbp;
 RX MEDLINE=87040747; PubMed=3774547;
 RA Fairweather N.F., Lyness V.A.;
 RT "The complete nucleotide sequence of tetanus toxin.";
 RL Nucleic Acids Res. 14:7809-7812(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Massachusetts / E88; PLASMID=pE88;
 RX MEDLINE=22457253; PubMed=12552129;
 RA Brueggemann H., Baeumer S., Fricke W.F., Wiezer A., Liesegang H.,
 RA Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
 RA Gottschalk G.;
 RT "The genome sequence of Clostridium tetani, the causative agent of
 RT tetanus disease.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).
 RN [4]
 RP SEQUENCE OF 742-1314 FROM N.A.
 RC PLASMID=75 Kbp;
 RX MEDLINE=86085672; PubMed=3510187;
 RA Fairweather N.F., Lyness V.A., Pickard D.J., Allen G., Thomson R.O.;
 RT "Cloning, nucleotide sequencing, and expression of tetanus toxin
 RT fragment C in Escherichia coli.";
 RL J. Bacteriol. 165:21-27(1986).
 RN [5]
 RP PARTIAL SEQUENCE, AND DISULFIDE BONDS.
 RX MEDLINE=90201034; PubMed=2108021;
 RA Krieglstein K., Henschen A., Weller U., Habermann E.;
 RT "Arrangement of disulfide bridges and positions of sulfhydryl groups
 RT in tetanus toxin.";
 RL Eur. J. Biochem. 188:39-45(1990).
 RN [6]
 RP PARTIAL SEQUENCE.
 RX MEDLINE=92037649; PubMed=1935979;
 RA Krieglstein K.G., Henschen A.H., Weller U., Habermann E.;
 RT "Limited proteolysis of tetanus toxin. Relation to activity and
 RT identification of cleavage sites.";
 RL Eur. J. Biochem. 202:41-51(1991).
 RN [7]
 RP IDENTIFICATION AS ZINC-PROTEASE.
 RX MEDLINE=93010948; PubMed=1396558;
 RA Schiavo G., Poulain B., Rossetto O., Benfenati F., Tauc L.,
 RA Montecucco C.;
 RT "Tetanus toxin is a zinc protein and its inhibition of
 RT neurotransmitter release and protease activity depend on zinc.";
 RL EMBO J. 11:3577-3583(1992).
 RN [8]
 RP IDENTIFICATION OF SUBSTRATE.
 RX MEDLINE=93063293; PubMed=1331807;
 RA Schiavo G., Benfenati F., Poulain B., Rossetto O., de Laureto P.P.,
 RA Dasgupta B.R., Montecucco C.;
 RT "Tetanus and botulinum-B neurotoxins block neurotransmitter release
 RT by proteolytic cleavage of synaptobrevin.";
 RL Nature 359:832-835(1992).
 RN [9]

RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 874-1314.
 RX MEDLINE=97475217; PubMed=9334741;
 RA Umland T.C., Wingert L.M., Swaminathan S., Furey W.F., Schmidt J.J.,
 RA Sax M.;
 RT "Structure of the receptor binding fragment HC of tetanus
 RT neurotoxin.";
 RL Nat. Struct. Biol. 4:788-792(1997).
 CC -!- FUNCTION: TETANUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
 CC RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
 CC AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
 CC WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
 CC INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
 CC ENDOPEPTIDASE THAT CATALYZES THE HYDROLYSIS OF THE 76-GLN-|-PHE-77
 CC BOND OF SYNAPTObREVIN-2.
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of 76-Gln-|-Phe-77 bond in
 CC synaptobrevin 2.
 CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -!- SUBUNIT: THE PRECURSOR POLYPEPTIDE IS SUBSEQUENTLY CLEAVED TO
 CC YIELD SUBCHAINS L AND H. THESE REMAIN LINKED BY A DISULFIDE BRIDGE
 CC AND ARE NON-TOXIC AFTER SEPARATION.
 CC -!- MISCELLANEOUS: THE C-TERMINAL OF THE HEAVY CHAIN BINDS TO
 CC GANGLIOSIDE RECEPTORS.
 CC -!- SIMILARITY: Belongs to peptidase family M27.
 CC -----
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 CC -----
 DR EMBL; X04436; CAA28033.1; -.
 DR EMBL; X06214; CAA29564.1; -.
 DR EMBL; AF528097; AAO37454.1; -.
 DR EMBL; M12739; AAA23282.1; -.
 DR PIR; A25689; BTCLTN.
 DR PDB; 1AF9; 29-APR-98.
 DR PDB; 1A8D; 14-OCT-98.
 DR PDB; 1D0H; 27-MAR-00.
 DR PDB; 1DFQ; 24-MAR-00.
 DR PDB; 1DIW; 24-MAR-00.
 DR PDB; 1DLL; 24-MAR-00.
 DR PDB; 1FV3; 05-SEP-01.
 DR MEROPS; M27.001; -.
 DR InterPro; IPR008985; ConA_like_lec_gl.
 DR InterPro; IPR002160; Kunitz_legume.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR000395; Peptidase_M27.
 DR Pfam; PF01742; Peptidase_M27; 1.
 DR PRINTS; PR00760; BONTOXILYSIN.
 DR ProDom; PD001963; Bontoxilysin; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KW Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc; Plasmid;
 KW 3D-structure; Complete proteome.
 FT INIT MET 0 0
 FT CHAIN 1 456 TETANUS TOXIN LIGHT CHAIN.

FT	CHAIN	457	1314
FT	METAL	232	232
FT	ACT_SITE	233	233
FT	METAL	236	236
FT	TRANSMEM	226	246
FT	TRANSMEM	669	689
FT	DISULFID	438	466
FT	DISULFID	1076	1092
FT	HELIX	876	882
FT	TURN	883	883
FT	STRAND	884	891
FT	TURN	892	893
FT	STRAND	894	897
FT	STRAND	904	907
FT	TURN	909	910
FT	STRAND	912	915
FT	STRAND	920	925
FT	TURN	928	929
FT	STRAND	932	935
FT	HELIX	938	940
FT	TURN	941	946
FT	STRAND	949	956
FT	HELIX	962	968
FT	TURN	969	970
FT	STRAND	972	977
FT	STRAND	980	981
FT	HELIX	983	985
FT	STRAND	987	995
FT	TURN	996	997
FT	STRAND	998	1004
FT	TURN	1006	1007
FT	STRAND	1010	1016
FT	STRAND	1020	1020
FT	TURN	1021	1022
FT	STRAND	1031	1037
FT	TURN	1039	1040
FT	STRAND	1042	1047
FT	TURN	1048	1049
FT	STRAND	1050	1056
FT	TURN	1058	1059
FT	STRAND	1068	1074
FT	TURN	1079	1080
FT	STRAND	1082	1091
FT	HELIX	1097	1105
FT	TURN	1106	1107
FT	STRAND	1112	1112
FT	STRAND	1114	1114
FT	TURN	1116	1117
FT	STRAND	1120	1120
FT	STRAND	1122	1122
FT	TURN	1123	1124
FT	STRAND	1127	1131
FT	HELIX	1132	1134
FT	TURN	1135	1136
FT	STRAND	1137	1141
FT	TURN	1144	1145
FT	STRAND	1148	1152

TETANUS TOXIN HEAVY CHAIN.
 ZINC (CATALYTIC) (BY SIMILARITY).
 BY SIMILARITY.
 ZINC (CATALYTIC) (BY SIMILARITY).
 POTENTIAL.
 POTENTIAL.
 INTERCHAIN.

FT	STRAND	1155	1158
FT	TURN	1159	1162
FT	STRAND	1163	1166
FT	STRAND	1173	1178
FT	TURN	1184	1185
FT	STRAND	1188	1188
FT	STRAND	1190	1190

Query Match 100.0%; Score 112; DB 1; Length 1314;
 Best Local Similarity 100.0%; Pred. No. 2.8e-10;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSEFWLRVPKVSASHLE 21
 |||||
 Db 946 FNNFTVSEFWLRVPKVSASHLE 966

RESULT 2

BXF_CLOBO

ID BXF_CLOBO STANDARD; PRT; 1274 AA.
 AC P30996;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Botulinum neurotoxin type F precursor (EC 3.4.24.69) (BoNT/F)
 DE (Bontoxilysin F).
 GN BOTF.
 OS Clostridium botulinum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 23387;
 RX MEDLINE=93012902; PubMed=1398040;
 RA East A.K., Richardson P.T., Allaway D., Collins M.D.,
 RA Roberts T.A., Thompson D.E.;
 RT "Sequence of the gene encoding type F neurotoxin of Clostridium
 RT botulinum.";
 RL FEMS Microbiol. Lett. 75:225-230(1992).
 RN [2]
 RP SEQUENCE OF 1-64 FROM N.A.
 RC STRAIN=Hobbs FT10;
 RX MEDLINE=94297488; PubMed=7764998;
 RA East A.K., Collins M.D.;
 RT "Conserved structure of genes encoding components of botulinum
 RT neurotoxin complex M and the sequence of the gene coding for the
 RT nontoxic component in nonproteolytic Clostridium botulinum type F.";
 RL Curr. Microbiol. 29:69-77(1994).
 RN [3]
 RP SEQUENCE OF 634-1002 FROM N.A.
 RX MEDLINE=94013372; PubMed=8408542;
 RA Campbell K., East A.K., Collins M.D.;
 RT "Gene probes for identification of the botulinal neurotoxin gene and
 RT specific identification of neurotoxin types B, E, and F.";
 RL J. Clin. Microbiol. 31:2255-2262(1993).
 RN [4]

RP IDENTIFICATION OF SUBSTRATE.
RX MEDLINE=94230352; PubMed=8175689;
RA Yamasaki S., Baumeister A., Binz T., Blasi J., Link E., Cornille F.,
RA Roques B., Fykse E.M., Suedhof T.C., Jahn R., Niemann H.;
RT "Cleavage of members of the synaptobrevin/VAMP family by types D and
RT F botulinum neurotoxins and tetanus toxin.";
RL J. Biol. Chem. 269:12764-12772(1994).
CC -!- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
CC RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
CC AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
CC WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
CC INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
CC ENDOPEPTIDASE THAT CATALYZES THE HYDROLYSIS OF THE 58-GLN-|-LYS-59
CC BOND OF SYNAPTOBREVINS-1 AND -2.
CC -!- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the
CC neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No
CC detected action on small molecule substrates.
CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -!- SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a
CC heavy chain (H). The light chain has the pharmacological activity,
CC while the N- and C-terminal of the heavy chain mediate channel
CC formation and toxin binding, respectively.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MISCELLANEOUS: There are seven antigenically distinct forms of
CC botulinum neurotoxin: Types A, B, C1, D, E, F, and G.
CC -!- SIMILARITY: Belongs to peptidase family M27.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M92906; AAA23263.1; -.
DR EMBL; S73676; AAC60475.1; -.
DR EMBL; X70820; CAA50151.1; -.
DR EMBL; X70816; CAA50147.1; -.
DR PIR; I40813; I40813.
DR PIR; S48109; S48109.
DR HSSP; P10845; 3BTA.
DR MEROPS; M27.002; -.
DR InterPro; IPR008985; ConA_like_lec_gl.
DR InterPro; IPR002160; Kunitz_legume.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR000395; Peptidase_M27.
DR Pfam; PF01742; Peptidase_M27; 1.
DR PRINTS; PR00760; BONTOTOXILYSIN.
DR ProDom; PD001963; Bontoxilysin; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc.
FT CHAIN 1 436 BOTULINUM NEUROTOXIN F, LIGHT-CHAIN.
FT CHAIN 437 1274 BOTULINUM NEUROTOXIN F, HEAVY-CHAIN.
FT METAL 227 227 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 228 228 BY SIMILARITY.
FT METAL 231 231 ZINC (CATALYTIC) (BY SIMILARITY).

FT DISULFID 429 445 INTERCHAIN (PROBABLE).
SQ SEQUENCE 1274 AA; 146709 MW; 5B99756A7438B921 CRC64;

Query Match 54.5%; Score 61; DB 1; Length 1274;
Best Local Similarity 57.1%; Pred. No. 0.065;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPK 14
: ||::|||:|:|
Db 930 YQNFSISFWVRIPK 943

RESULT 3

BXG_CLOBO

ID BXG_CLOBO STANDARD; PRT; 1296 AA.
AC Q60393;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Botulinum neurotoxin type G precursor (EC 3.4.24.69) (BoNT/G)
DE (Bontoxilysin G).
GN BOTG.
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=113 / 30;
RX MEDLINE=94092745; PubMed=8268233;
RA Campbell K., Collins M.D., East A.K.;
RT "Nucleotide sequence of the gene coding for Clostridium botulinum
RT (Clostridium argentinense) type G neurotoxin: genealogical comparison
RT with other clostridial neurotoxins."
RL Biochim. Biophys. Acta 1216:487-491(1993).
CC -!- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
CC RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
CC AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
CC WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
CC INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
CC ENDOPEPTIDASE.
CC -!- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the
CC neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No
CC detected action on small molecule substrates.
CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -!- SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a
CC heavy chain (H). The light chain has the pharmacological activity,
CC while the N- and C-terminal of the heavy chain mediate channel
CC formation and toxin binding, respectively.
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- MISCELLANEOUS: There are seven antigenically distinct forms of
CC botulinum neurotoxin: Types A, B, C1, D, E, F, and G.
CC -!- SIMILARITY: Belongs to peptidase family M27.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its

RT neurotoxin, deduced by nucleotide sequence analysis of the encoding
 RT gene.";
 RL Eur. J. Biochem. 189:73-81(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=62A;
 RX MEDLINE=90264400; PubMed=2160960;
 RA Binz B., Kuarazono H., Wille M., Frevent J., Wernars K., Niemann H.;
 RT "The complete sequence of botulinum neurotoxin type A and comparison
 RT with other clostridial neurotoxins.";
 RL J. Biol. Chem. 265:9153-9158(1990).
 RN [3]
 RP SEQUENCE OF 1-65 FROM N.A.
 RC STRAIN=62A;
 RX MEDLINE=97016817; PubMed=8863443;
 RA East A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;
 RT "Organization and phylogenetic interrelationships of genes encoding
 RT components of the botulinum toxin complex in proteolytic Clostridium
 RT botulinum types A, B, and F: evidence of chimeric sequences in the
 RT gene encoding the nontoxic nonhemagglutinin component.";
 RL Int. J. Syst. Bacteriol. 46:1105-1112(1996).
 RN [4]
 RP SEQUENCE OF 1-34 FROM N.A.
 RC STRAIN=Hall;
 RX MEDLINE=89350959; PubMed=2669749;
 RA Betley M.J., Somers E., Dasgupta B.R.;
 RT "Characterization of botulinum type A neurotoxin gene: delineation of
 RT the N-terminal encoding region.";
 RL Biochem. Biophys. Res. Commun. 162:1388-1395(1989).
 RN [5]
 RP SEQUENCE OF 1-18 FROM N.A.
 RC STRAIN=Type A NIH;
 RX MEDLINE=96096783; PubMed=8521962;
 RA Fujita R., Fujinaga Y., Inoue K., Nakajima H., Kumon H., Oguma K.;
 RT "Molecular characterization of two forms of nontoxic-nonhemagglutinin
 RT components of Clostridium botulinum type A progenitor toxins.";
 RL FEBS Lett. 376:41-44(1995).
 RN [6]
 RP SEQUENCE OF 1-16.
 RX MEDLINE=84178501; PubMed=6370252;
 RA Schmidt J.J., Sartymoorthy V., Dasgupta B.R.;
 RT "Partial amino acid sequence of the heavy and light chains of
 RT botulinum neurotoxin type A.";
 RL Biochem. Biophys. Res. Commun. 119:900-904(1984).
 RN [7]
 RP SEQUENCE OF 1-46.
 RA Dasgupta B.R., Foley J., Niece R.;
 RT "Partial sequence of the light chain of botulinum neurotoxin type A.";
 RL Biochemistry 26:4162-4162(1987).
 RN [8]
 RP SEQUENCE OF 1-5 AND 444-456.
 RX MEDLINE=91120847; PubMed=2126206;
 RA Dasgupta B.R., Dekleva M.L.;
 RT "Botulinum neurotoxin type A: sequence of amino acids at the
 RT N-terminus and around the nicking site.";
 RL Biochimie 72:661-664(1990).
 RN [9]

RP SEQUENCE OF 448-464 AND 872-895.
 RX MEDLINE=89024662; PubMed=3178218;
 RA Sathymoorthy V., Dasgupta B.R., Foley J., Niece R.L.;
 RT "Botulinum neurotoxin type A: cleavage of the heavy chain into two
 RT halves and their partial sequences.";
 RL Arch. Biochem. Biophys. 266:142-151(1988).
 RN [10]
 RP SEQUENCE OF 448-482.
 RX MEDLINE=85285016; PubMed=3896784;
 RA Shone C.C., Hambleton P., Melling J.;
 RT "Inactivation of Clostridium botulinum type A neurotoxin by trypsin
 RT and purification of two tryptic fragments. Proteolytic action near
 RT the COOH-terminus of the heavy subunit destroys toxin-binding
 RT activity.";
 RL Eur. J. Biochem. 151:75-82(1985).
 RN [11]
 RP IDENTIFICATION OF SUBSTRATE.
 RX MEDLINE=94063091; PubMed=8243676;
 RA Schiavo G., Santtuci A., Dasgupta B.R., Mehta P.P., Jontes J.,
 RA Benfenati F., Wilson M.C., Montecucco C.;
 RT "Botulinum neurotoxins serotypes A and E cleave SNAP-25 at distinct
 RT COOH-terminal peptide bonds.";
 RL FEBS Lett. 335:99-103(1993).
 RN [12]
 RP IDENTIFICATION OF SUBSTRATE.
 RX MEDLINE=94124495; PubMed=8294407;
 RA Binz T., Blasi J., Yamasaki S., Baumeister A., Link E., Suedhof T.C.,
 RA Jahn R., Niemann H.;
 RT "Proteolysis of SNAP-25 by types E and A botulinum neurotoxins.";
 RL J. Biol. Chem. 269:1617-1620(1994).
 RN [13]
 RP MUTAGENESIS OF GLU-261; PHE-265 AND TYR-365.
 RX MEDLINE=21556941; PubMed=11700044;
 RA Rigoni M., Caccin P., Johnson E.A., Montecucco C., Rossetto O.;
 RT "Site-directed mutagenesis identifies active-site residues of the
 RT light chain of botulinum neurotoxin type a.";
 RL Biochem. Biophys. Res. Commun. 288:1231-1237(2001).
 RN [14]
 RP X-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS).
 RX MEDLINE=98455071; PubMed=9783750;
 RA Lacy D.B., Tepp W., Cohen A.C., Dasgupta B.R., Stevens R.C.;
 RT "Crystal structure of botulinum neurotoxin type A and implications
 RT for toxicity.";
 RL Nat. Struct. Biol. 5:898-902(1998).
 CC -!- FUNCTION: Inhibits acetylcholine release. The botulinum toxin
 CC binds with high affinity to peripheral neuronal presynaptic
 CC membrane, is then internalized by receptor-mediated endocytosis.
 CC The C-terminus of the heavy chain (H) is responsible for the
 CC adherence of the toxin to the cell surface while the N-terminus
 CC mediates transport of the light chain from the endocytic vesicle
 CC to the cytosol. After translocation, the light chain (L)
 CC hydrolyzes the 197-Gln-|-Arg-198 bond in SNAP-25, thereby blocking
 CC neurotransmitter release. Inhibition of acetylcholine release
 CC results in flaccid paralysis, with frequent heart or respiratory
 CC failure.
 CC -!- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the
 CC neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No

CC detected action on small molecule substrates.
 CC -!- COFACTOR: Binds 1 zinc ion per subunit.
 CC -!- SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a
 CC heavy chain (H).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PHARMACEUTICAL: Available under the name BOTOX (Allergan) for
 CC the treatment of strabismus and blepharospasm associated with
 CC dystonia and cervical dystonia. Also used for the treatment of
 CC hemifacial spasm and a number of other neurological disorders
 CC characterized by abnormal muscle contraction.
 CC -!- MISCELLANEOUS: There are seven antigenically distinct forms of
 CC botulinum neurotoxin: Types A, B, C1, D, E, F, and G.
 CC -!- SIMILARITY: Belongs to peptidase family M27.
 CC -!- DATABASE: NAME=BOTOX product information Web site;
 CC WWW="http://www.botox.com/index.jsp?hp&productinfo".
 CC -!- DATABASE: NAME=Protein Spotlight;
 CC NOTE=Issue 19 of February 2002;
 CC WWW="http://www.expasy.org/spotlight/articles/sptlt019.html".

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 CC -----

DR EMBL; X52066; CAA36289.1; -.
 DR EMBL; M30196; AAA23262.1; -.
 DR EMBL; X92973; CAA63551.1; -.
 DR EMBL; D67030; BAA11051.1; -.
 DR EMBL; M27892; AAA23269.1; -.
 DR PIR; A35294; BTCLAB.
 DR PDB; 3BTA; 01-OCT-99.
 DR MEROPS; M27.002; -.
 DR InterPro; IPR008985; ConA_like_lec_gl.
 DR InterPro; IPR002160; Kunitz_legume.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR000395; Peptidase_M27.
 DR Pfam; PF01742; Peptidase_M27; 1.
 DR PRINTS; PR00760; BONTOXILYSIN.
 DR ProDom; PD001963; Bontoxilysin; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KW Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc;
 KW Pharmaceutical; 3D-structure.
 FT INIT_MET 0 0
 FT CHAIN 1 447 BOTULINUM NEUROTOXIN A, LIGHT-CHAIN.
 FT CHAIN 448 1295 BOTULINUM NEUROTOXIN A, HEAVY-CHAIN.
 FT METAL 222 222 ZINC (CATALYTIC).
 FT ACT_SITE 223 223
 FT METAL 226 226 ZINC (CATALYTIC).
 FT METAL 261 261 ZINC (CATALYTIC).
 FT DISULFID 429 453 INTERCHAIN.
 FT DISULFID 1234 1279
 FT TRANSMEM 626 646 POTENTIAL.
 FT TRANSMEM 655 675 POTENTIAL.
 FT VARIANT 26 26 V -> A.

FT	MUTAGEN	261	261	E->A: DRASTIC DECREASE IN ENZYMATI
FT				ACTIVITY.
FT	MUTAGEN	265	265	F->A: DECREASES ENZYMATI
FT	MUTAGEN	365	365	Y->A: DECREASES ENZYMATI
FT	CONFLICT	1	1	P -> Q (IN REF. 1).
FT	CONFLICT	479	479	E -> P (IN REF. 9).
FT	CONFLICT	875	875	T -> L (IN REF. 8).
FT	CONFLICT	891	891	S -> K (IN REF. 8).
SQ	SEQUENCE	1295 AA; 149322 MW; 858342F754862579 CRC64;		

Query Match 52.7%; Score 59; DB 1; Length 1295;
 Best Local Similarity 57.1%; Pred. No. 0.14;
 Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FNNFTVSEFWLRVPK 14
 : ||: |||:|:|
 Db 937 YENFSTSEFWIRIPK 950

RESULT 5

BXB_CLOBO

ID BXB_CLOBO STANDARD; PRT; 1290 AA.
 AC P10844; P10843;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Botulinum neurotoxin type B precursor (EC 3.4.24.69) (BoNT/B)
 DE (Bontoxilysin B).
 GN BOTB.
 OS Clostridium botulinum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92384550; PubMed=1514783;
 RA Whelan S.M., Elmore M.J., Bodsworth N.J., Brehm J.K., Atkinson T.,
 RA Minton N.P.;
 RT "Molecular cloning of the Clostridium botulinum structural gene
 RT encoding the type B neurotoxin and determination of its entire
 RT nucleotide sequence.";
 RL Appl. Environ. Microbiol. 58:2345-2354(1992).
 RN [2]
 RP SEQUENCE OF 35-245 FROM N.A.
 RC STRAIN=NCTC 7273;
 RA Szabo E.A., Pemberton J.M., Desmarchelier P.M.;
 RL Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE OF 633-993 FROM N.A.
 RC STRAIN=NCTC 7273;
 RX MEDLINE=94013372; PubMed=8408542;
 RA Campbell K., East A.K., Collins M.D.;
 RT "Gene probes for identification of the botulinal neurotoxin gene and
 RT specific identification of neurotoxin types B, E, and F.";
 RL J. Clin. Microbiol. 31:2255-2262(1993).
 RN [4]
 RP SEQUENCE OF 1-44 AND 441-466.

RC STRAIN=657;
 RX MEDLINE=89000987; PubMed=3139097;
 RA Dasgupta B.R., Datta A.;
 RT "Botulinum neurotoxin type B (strain 657): partial sequence and
 RT similarity with tetanus toxin.";
 RL Biochimie 70:811-817(1988).
 RN [5]
 RP SEQUENCE OF 1-16 AND 441-458.
 RC STRAIN=OKRA;
 RX MEDLINE=85197963; PubMed=3888113;
 RA Schmidt J.J., Sathyamoorthy V., Dasgupta B.R.;
 RT "Partial amino acid sequences of botulinum neurotoxins types B and
 RT E.";
 RL Arch. Biochem. Biophys. 238:544-548(1985).
 RN [6]
 RP IDENTIFICATION AS ZINC-PROTEASE.
 RX MEDLINE=93054694; PubMed=1429690;
 RA Schiavo G., Rossetto O., Santucci A., Dasgupta B.R., Montecucco C.;
 RT "Botulinum neurotoxins are zinc proteins.";
 RL J. Biol. Chem. 267:23479-23483(1992).
 RN [7]
 RP IDENTIFICATION OF SUBSTRATE.
 RX MEDLINE=93063293; PubMed=1331807;
 RA Schiavo G., Benfenati F., Poulain B., Rossetto O., de Laureto P.P.,
 RA Dasgupta B.R., Montecucco C.;
 RT "Tetanus and botulinum-B neurotoxins block neurotransmitter release
 RT by proteolytic cleavage of synaptobrevin.";
 RL Nature 359:832-835(1992).
 CC -!- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
 CC RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
 CC AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
 CC WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
 CC INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
 CC ENDOPEPTIDASE THAT CLEAVES THE 76-GLN-|-PHE-77 BOND OF
 CC SYNAPTOBREVIN-2.
 CC -!- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the
 CC neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No
 CC detected action on small molecule substrates.
 CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -!- SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a
 CC heavy chain (H). The light chain has the pharmacological activity,
 CC while the N- and C-terminal of the heavy chain mediate channel
 CC formation and toxin binding, respectively.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MISCELLANEOUS: There are seven antigenically distinct forms of
 CC botulinum neurotoxin: Types A, B, C1, D, E, F, and G.
 CC -!- SIMILARITY: Belongs to peptidase family M27.
 CC -----
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 CC -----
 DR EMBL; M81186; AAA23211.1; -.

DR EMBL; Z11934; CAA77991.1; -.
 DR EMBL; X70817; CAA50148.1; -.
 DR PIR; A48940; A48940.
 DR PDB; 1EPW; 01-NOV-00.
 DR PDB; 1F31; 01-NOV-00.
 DR PDB; 1F82; 16-AUG-00.
 DR PDB; 1F83; 16-AUG-00.
 DR PDB; 1FQH; 06-DEC-00.
 DR PDB; 1G9A; 13-NOV-02.
 DR PDB; 1G9B; 13-NOV-02.
 DR PDB; 1G9C; 13-NOV-02.
 DR PDB; 1G9D; 13-NOV-02.
 DR PDB; 1I1E; 21-NOV-01.
 DR MEROPS; M27.002; -.
 DR InterPro; IPR008985; ConA_like_lec_gl.
 DR InterPro; IPR002160; Kunitz_legume.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR000395; Peptidase_M27.
 DR Pfam; PF01742; Peptidase_M27; 1.
 DR PRINTS; PR00760; BONTOXILYSIN.
 DR ProDom; PD001963; Bontoxilysin; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KW Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc;
 KW 3D-structure.
 FT INIT_MET 0 0
 FT CHAIN 1 440 BOTULINUM NEUROTOXIN B, LIGHT-CHAIN.
 FT CHAIN 441 1290 BOTULINUM NEUROTOXIN B, HEAVY-CHAIN.
 FT METAL 229 229 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACT_SITE 230 230 BY SIMILARITY.
 FT METAL 233 233 ZINC (CATALYTIC) (BY SIMILARITY).
 FT DISULFID 436 445 INTERCHAIN (PROBABLE).
 FT CONFLICT 29 29 T -> M (IN REF. 4).
 FT CONFLICT 217 217 R -> G (IN REF. 2).
 FT CONFLICT 224 224 A -> S (IN REF. 2).
 FT CONFLICT 463 463 S -> R (IN REF. 4).
 SQ SEQUENCE 1290 AA; 150670 MW; D21746E2C024DF43 CRC64;

Query Match 51.8%; Score 58; DB 1; Length 1290;
 Best Local Similarity 64.3%; Pred. No. 0.21;
 Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 FNNFTVSEFWLRVPK 14
 | :|:||||:|:|
 Db 922 FLDFSVSEFWIRIPK 935

RESULT 6

VP2_AHSV6

ID VP2_AHSV6 STANDARD; PRT; 1051 AA.
 AC 071024;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Outer capsid protein VP2.
 GN S2 OR L2.
 OS African horse sickness virus 6 (AHSV-6) (African horse sickness virus
 OS (serotype 6)).

OC Viruses; dsRNA viruses; Reoviridae; Orbivirus.
 OX NCBI_TaxID=86060;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98278331; PubMed=9617769;
 RA Williams C.F., Inoue T., Lucus A.-M., Zanotto P., Roy P.;
 RT "The complete sequence of four major structural proteins of African
 RT horse sickness virus serotype 6: evolutionary relationships within
 RT and between the orbiviruses."
 RL Virus Res. 53:53-73(1998).
 CC -!- FUNCTION: THE VP2 PROTEIN IS ONE OF THE TWO PROTEINS (WITH VP5)
 CC WHICH CONSTITUTE THE VIRUS PARTICLE OUTER CAPSID. IT IS THE
 CC MAJOR TARGET OF THE HOST IMMUNOGENIC RESPONSE.
 CC -!- SIMILARITY: Belongs to the reoviruses VP2 protein family.
 CC -----
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 CC -----
 DR EMBL; AF021235; AAC40994.1; -.
 DR InterPro; IPR001742; Orbi_VP2.
 DR Pfam; PF00898; Orbi_VP2; 1.
 KW Coat protein.
 SQ SEQUENCE 1051 AA; 122326 MW; 2B04DB9E389F4B5F CRC64;

Query Match 50.9%; Score 57; DB 1; Length 1051;
 Best Local Similarity 47.6%; Pred. No. 0.24;
 Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 FNNFTVSEFWLRVPKVSASHLE 21
 |: ||:| || |:| |||
 Db 636 FSKRFVSYWYRVEKITTKHLE 656

RESULT 7

BXE_CLOBO

ID BXE_CLOBO STANDARD; PRT; 1250 AA.
 AC Q00496;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Botulinum neurotoxin type E precursor (EC 3.4.24.69) (BoNT/E)
 DE (Bontoxilysin E).
 OS Clostridium botulinum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Beluga;
 RX MEDLINE=92181428; PubMed=1543481;
 RA Poulet S., Hauser D., Quanz M., Niemann H., Popoff M.R.;
 RT "Sequences of the botulinal neurotoxin E derived from Clostridium

RT botulinum type E (strain Beluga) and Clostridium butyricum (strains
 RT ATCC 43181 and ATCC 43755).";
 RL Biochem. Biophys. Res. Commun. 183:107-113(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92174922; PubMed=1541280;
 RA Whelan S.M., Elmore M.J., Bodsworth N.J., Atkinson T., Minton N.P.;
 RT "The complete amino acid sequence of the Clostridium botulinum type-E
 RT neurotoxin, derived by nucleotide-sequence analysis of the encoding
 RT gene.";
 RL Eur. J. Biochem. 204:657-667(1992).
 RN [3]
 RP SEQUENCE OF 1-251 FROM N.A.
 RX MEDLINE=90264400; PubMed=2160960;
 RA Binz T., Kurazono H., Wille M., Frevert J., Wernars K., Niemann H.;
 RT "The complete sequence of botulinum neurotoxin type A and comparison
 RT with other clostridial neurotoxins.";
 RL J. Biol. Chem. 265:9153-9158(1990).
 RN [4]
 RP SEQUENCE OF 1-13.
 RX MEDLINE=85197963; PubMed=3888113;
 RA Schmidt J.J., Sathyamoorthy V., Dasgupta B.R.;
 RT "Partial amino acid sequences of botulinum neurotoxins types B and
 RT E.";
 RL Arch. Biochem. Biophys. 238:544-548(1985).
 RN [5]
 RP SEQUENCE OF 419-426.
 RX MEDLINE=90344918; PubMed=2116911;
 RA Gimenez J.A., Dasgupta B.R.;
 RT "Botulinum neurotoxin type E fragmented with endoproteinase Lys-C
 RT reveals the site trypsin nicks and homology with tetanus
 RT neurotoxin.";
 RL Biochimie 72:213-217(1990).
 RN [6]
 RP IDENTIFICATION OF SUBSTRATE.
 RX MEDLINE=94063091; PubMed=8243676;
 RA Schiavo G., Santtuci A., Dasgupta B.R., Mehta P.P., Jontes J.,
 RA Benfenati F., Wilson M.C., Montecucco C.;
 RT "Botulinum neurotoxins serotypes A and E cleave SNAP-25 at distinct
 RT COOH-terminal peptide bonds.";
 RL FEBS Lett. 335:99-103(1993).
 RN [7]
 RP IDENTIFICATION OF SUBSTRATE.
 RX MEDLINE=94124495; PubMed=8294407;
 RA Binz T., Blasi J., Yamasaki S., Baumeister A., Link E., Suedhof T.C.,
 RA Jahn R., Niemann H.;
 RT "Proteolysis of SNAP-25 by types E and A botulinal neurotoxins.";
 RL J. Biol. Chem. 269:1617-1620(1994).
 CC -!- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
 CC RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
 CC AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
 CC WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
 CC INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
 CC ENDOPEPTIDASE THAT CATALYZES THE HYDROLYSIS OF THE 180-ARG-|-ILE-
 CC 181 BOND IN SNAP-25.
 CC -!- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the
 CC neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No

CC detected action on small molecule substrates.
 CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -!- SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a
 CC heavy chain (H). The light chain has the pharmacological activity,
 CC while the N- and C-terminal of the heavy chain mediate channel
 CC formation and toxin binding, respectively.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MISCELLANEOUS: There are seven antigenically distinct forms of
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 CC -!- SIMILARITY: Belongs to peptidase family M27.
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 CC -----
 DR EMBL; X62089; CAA43999.1; -.
 DR EMBL; X62683; CAA44558.1; -.
 DR PIR; S08575; S08575.
 DR PIR; S21178; S21178.
 DR HSSP; P10845; 3BTA.
 DR MEROPS; M27.002; -.
 DR InterPro; IPR008985; ConA_like_lec_gl.
 DR InterPro; IPR002160; Kunitz_legume.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR000395; Peptidase_M27.
 DR Pfam; PF01742; Peptidase_M27; 1.
 DR PRINTS; PR00760; BONTOXILYSIN.
 DR ProDom; PD001963; Bontoxilysin; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KW Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc.
 FT INIT_MET 0 0
 FT CHAIN 1 421 BOTULINUM NEUROTOXIN E, LIGHT-CHAIN.
 FT CHAIN 422 1250 BOTULINUM NEUROTOXIN E, HEAVY-CHAIN.
 FT METAL 211 211 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACT_SITE 212 212 BY SIMILARITY.
 FT METAL 215 215 ZINC (CATALYTIC) (BY SIMILARITY).
 FT DISULFID 411 425 INTERCHAIN (PROBABLE).
 FT CONFLICT 176 176 R -> G (IN REF. 2).
 FT CONFLICT 197 197 C -> S (IN REF. 2 AND 3).
 FT CONFLICT 339 339 R -> A (IN REF. 2).
 FT CONFLICT 772 772 I -> L (IN REF. 2).
 FT CONFLICT 962 963 FE -> LQ (IN REF. 2).
 FT CONFLICT 966 966 R -> A (IN REF. 2).
 FT CONFLICT 1194 1194 N -> NN (IN REF. 2).
 SQ SEQUENCE 1250 AA; 143712 MW; D9FCE26DDA041EB4 CRC64;

Query Match 50.0%; Score 56; DB 1; Length 1250;
 Best Local Similarity 53.8%; Pred. No. 0.42;
 Matches 7; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVP 13
 : ||::|||:|:|
 Db 911 YKNFSISFWVRIP 923

RESULT 8

BXE_CLOBU

ID BXE_CLOBU STANDARD; PRT; 1250 AA.
AC P30995;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Botulinum neurotoxin type E precursor (EC 3.4.24.69) (BoNT/E)
DE (Bontoxilysin E).
OS Clostridium butyricum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1492;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 43181, and ATCC 43755;
RX MEDLINE=92181428; PubMed=1543481;
RA Poulet S., Hauser D., Quanz M., Niemann H., Popoff M.R.;
RT "Sequences of the botulinal neurotoxin E derived from Clostridium
RT botulinum type E (strain Beluga) and Clostridium butyricum (strains
RT ATCC 43181 and ATCC 43755).";
RL Biochem. Biophys. Res. Commun. 183:107-113(1992).
RN [2]
RP SEQUENCE OF 1-251 FROM N.A.
RC STRAIN=BL6340;
RX MEDLINE=91237316; PubMed=2033376;
RA Fujii N., Kimura K., Murakami T., Indoh T., Tsuzuki K.,
RA Yokosawa N., Yashiki T., Oguma K.;
RT "Cloning of a DNA fragment encoding the 5'-terminus of the botulinum
RT type E toxin gene from Clostridium butyricum strain BL6340.";
RL J. Gen. Microbiol. 137:519-525(1991).
RN [3]
RP SEQUENCE OF 1-48.
RC STRAIN=5262;
RA Gimenez J., Foley J., Dasgupta B.R.;
RT "Neurotoxin type E from Clostridium botulinum and C. butyricum;
RT partial sequence and comparison.";
RL FASEB J. 2:A1750-A1750(1988).
CC -!- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
CC RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
CC AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
CC WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
CC INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
CC ENDOPEPTIDASE.
CC -!- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the
CC neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No
CC detected action on small molecule substrates.
CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -!- SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a
CC heavy chain (H). The light chain has the pharmacological activity,
CC while the N- and C-terminal of the heavy chain mediate channel
CC formation and toxin binding, respectively.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MISCELLANEOUS: There are seven antigenically distinct forms of
CC botulinum neurotoxin: Types A, B, C1, D, E, F, and G.

CC -!- SIMILARITY: Belongs to peptidase family M27.

CC -----

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CC -----

DR EMBL; X62088; CAA43998.1; -.
 DR EMBL; X53180; CAA37321.1; -.
 DR PIR; JH0256; JH0256.
 DR HSSP; P10845; 3BTA.
 DR MEROPS; M27.002; -.
 DR InterPro; IPR008985; ConA_like_lec_gl.
 DR InterPro; IPR002160; Kunitz_legume.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR000395; Peptidase_M27.
 DR Pfam; PF01742; Peptidase_M27; 1.
 DR PRINTS; PR00760; BONTOLILYSIN.
 DR ProDom; PD001963; Bontoxilysin; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KW Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc.
 FT INIT_MET 0 0
 FT CHAIN 1 421 BOTULINUM NEUROTOXIN E, LIGHT-CHAIN.
 FT CHAIN 422 1250 BOTULINUM NEUROTOXIN E, HEAVY-CHAIN.
 FT METAL 211 211 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACT_SITE 212 212 BY SIMILARITY.
 FT METAL 215 215 ZINC (CATALYTIC) (BY SIMILARITY).
 FT DISULFID 411 425 INTERCHAIN (PROBABLE).
 FT CONFLICT 229 229 K -> M (IN REF. 2).
 SQ SEQUENCE 1250 AA; 143265 MW; 8171B5B2C2312857 CRC64;

Query Match 50.0%; Score 56; DB 1; Length 1250;
 Best Local Similarity 53.8%; Pred. No. 0.42;
 Matches 7; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVP 13
 : ||::|||:|:|
 Db 911 YKNFSISFWVRIP 923

RESULT 9

BXA2_CLOBO

ID BXA2_CLOBO STANDARD; PRT; 1295 AA.
 AC Q45894; P77780;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Botulinum neurotoxin type A precursor (EC 3.4.24.69) (BoNT/A)
 DE (Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin A, light-
 DE chain; Botulinum neurotoxin A, heavy-chain].
 GN BOTA OR BNA OR ATX.
 OS Clostridium botulinum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.

OX NCBI_TaxID=1491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Kyoto-F;
 RX MEDLINE=94143603; PubMed=8310180;
 RA Willems A., East A.K., Lawson P.A., Collins M.D.;
 RT "Sequence of the gene coding for the neurotoxin of Clostridium
 RT botulinum type A associated with infant botulism: comparison with
 RT other clostridial neurotoxins.";
 RL Res. Microbiol. 144:547-556(1993).
 RN [2]
 RP SEQUENCE OF 1-65 FROM N.A.
 RC STRAIN=Kyoto-F;
 RX MEDLINE=97016817; PubMed=8863443;
 RA East A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;
 RT "Organization and phylogenetic interrelationships of genes encoding
 RT components of the botulinum toxin complex in proteolytic Clostridium
 RT botulinum types A, B, and F: evidence of chimeric sequences in the
 RT gene encoding the nontoxic nonhemagglutinin component.";
 RL Int. J. Syst. Bacteriol. 46:1105-1112(1996).
 CC -!- FUNCTION: Inhibits acetylcholine release. The botulinum toxin
 CC binds with high affinity to peripheral neuronal presynaptic
 CC membrane, is then internalized by receptor-mediated endocytosis.
 CC The C-terminus of the heavy chain (H) is responsible for the
 CC adherence of the toxin to the cell surface while the N-terminus
 CC mediates transport of the light chain from the endocytic vesicle
 CC to the cytosol. After translocation, the light chain (L)
 CC hydrolyzes the 197-Gln-|-Arg-198 bond in SNAP-25, thereby blocking
 CC neurotransmitter release. Inhibition of acetylcholine release
 CC results in flaccid paralysis, with frequent heart or respiratory
 CC failure (By similarity).
 CC -!- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the
 CC neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No
 CC detected action on small molecule substrates.
 CC -!- SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a
 CC heavy chain (H) (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MISCELLANEOUS: There are seven antigenically distinct forms of
 CC botulinum neurotoxin: Types A, B, C1, D, E, F, and G.
 CC -!- SIMILARITY: Belongs to peptidase family M27.
 CC -----
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 CC -----
 DR EMBL; X73423; CAA51824.1; -.
 DR EMBL; X87974; CAA61234.1; -.
 DR PIR; I40645; I40645.
 DR HSSP; P10845; 3BTA.
 DR MEROPS; M27.002; -.
 DR InterPro; IPR008985; ConA_like_lec_gl.
 DR InterPro; IPR002160; Kunitz_legume.
 DR InterPro; IPR006025; Pept_M_Zn_BS.

DR InterPro; IPR000395; Peptidase_M27.
 DR Pfam; PF01742; Peptidase_M27; 1.
 DR PRINTS; PR00760; BONTOXILYSIN.
 DR ProDom; PD001963; Bontoxilysin; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
 KW Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT CHAIN 1 447 BOTULINUM NEUROTOXIN A, LIGHT-CHAIN.
 FT CHAIN 448 1295 BOTULINUM NEUROTOXIN A, HEAVY-CHAIN.
 FT METAL 222 222 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACT_SITE 223 223 BY SIMILARITY.
 FT METAL 226 226 ZINC (CATALYTIC) (BY SIMILARITY).
 FT DISULFID 429 453 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 1234 1279 BY SIMILARITY.
 FT TRANSMEM 626 646 POTENTIAL.
 FT TRANSMEM 655 675 POTENTIAL.
 SQ SEQUENCE 1295 AA; 149279 MW; 5DA04A13D98D6372 CRC64;

Query Match 50.0%; Score 56; DB 1; Length 1295;
 Best Local Similarity 50.0%; Pred. No. 0.44;
 Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPK 14
 : ||: |||:::|
 Db 937 YENFSTSEFWIKIPK 950

RESULT 10

VNSS_INSVN

ID VNSS_INSVN STANDARD; PRT; 449 AA.
 AC Q01811;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE Nonstructural protein NS-S.
 GN NSS.
 OS Impatiens necrotic spot virus (strain NL-07) (INSV).
 OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Tospovirus.
 OX NCBI_TaxID=31622;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92331780; PubMed=1385787;
 RA de Haan P., de Avila A.C., Kormelink R., Westerbroek A.,
 RA Gielen J.J., Peters D., Goldbach R.;
 RT "The nucleotide sequence of the S RNA of Impatiens necrotic spot
 RT virus, a novel tospovirus."
 RL FEBS Lett. 306:27-32(1992).
 CC -!- FUNCTION: Forms filamentous inclusion bodies.
 CC -----
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 CC -----

DR EMBL; X66972; CAA47382.1; -.
DR PIR; S23158; S23158.
DR InterPro; IPR004915; Bunya_NS-S_2.
DR Pfam; PF03231; Bunya_NS-S_2; 1.
KW Nonstructural protein.
SQ SEQUENCE 449 AA; 51197 MW; C46AC1372B114CA5 CRC64;

Query Match 46.4%; Score 52; DB 1; Length 449;
Best Local Similarity 45.0%; Pred. No. 0.65;
Matches 9; Conservative 5; Mismatches 4; Indels 2; Gaps 1;

Qy 2 NN--FTVSEFWLRVPKVSASH 19
|| | :| |:|:|: | :
Db 240 NNKPFKISLWMRIPKIMKSN 259

RESULT 11

VNSS_TSWV1

ID VNSS_TSWV1 STANDARD; PRT; 464 AA.
AC P26002;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Nonstructural protein NS-S.
GN NSS.
OS Tomato spotted wilt virus (strain Brazilian Br-01) (TSWV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Tospovirus.
OX NCBI_TaxID=36413;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90264829; PubMed=1693160;
RA de Haan P., Wagemakers L., Peters D., Goldbach R.;
RT "The S RNA segment of tomato spotted wilt virus has an ambisense
RT character.";
RL J. Gen. Virol. 71:1001-1007(1990).
CC -!- FUNCTION: Forms filamentous inclusion bodies.
CC -----
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CC -----
DR EMBL; D00645; BAA00540.1; -.
DR PIR; JQ0547; MNVUWC.
DR InterPro; IPR004915; Bunya_NS-S_2.
DR Pfam; PF03231; Bunya_NS-S_2; 1.
KW Nonstructural protein.
SQ SEQUENCE 464 AA; 52448 MW; AE5519179F9EF377 CRC64;

Query Match 46.4%; Score 52; DB 1; Length 464;
Best Local Similarity 64.3%; Pred. No. 0.67;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NNFTVSEFWLRVPKV 15

Db ::| :| |||||
239 SHFKLSLWLRVPKV 252

RESULT 12

VNSS_TSWVL

ID VNSS_TSWVL STANDARD; PRT; 467 AA.
AC P26003;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Nonstructural protein NS-S.
GN NSS.
OS Tomato spotted wilt virus (strain Bulgarian L3) (TSWV).
OC Viruses; ssRNA negative-strand viruses; Bunyaviridae; Tospovirus.
OX NCBI_TaxID=36415;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91132150; PubMed=1993884;
RA Maiss E., Ivanova L., Breyel E., Adam G.;
RT "Cloning and sequencing of the S RNA from a Bulgarian isolate of
RT tomato spotted wilt virus."
RL J. Gen. Virol. 72:461-464(1991).
CC -!- FUNCTION: Forms filamentous inclusion bodies.
CC -----
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CC -----
DR EMBL; D13926; BAA03024.1; -.
DR PIR; JQ0954; MNVUW1.
DR InterPro; IPR004915; Bunya_NS-S_2.
DR Pfam; PF03231; Bunya_NS-S_2; 1.
KW Nonstructural protein.
SQ SEQUENCE 467 AA; 52413 MW; 38E5CA4E802DB6DC CRC64;

Query Match 46.4%; Score 52; DB 1; Length 467;
Best Local Similarity 64.3%; Pred. No. 0.67;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NNFTVSFWLRVPKV 15
 ::| :| |||||
Db 243 SHFKLSLWLRVPKV 256

RESULT 13

BXCN_CLOBO

ID BXCN_CLOBO STANDARD; PRT; 1196 AA.
AC P46081;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Botulinum neurotoxin type C1, nontoxic component.

OS Clostridium botulinum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Type C Stockholm / C-ST;
 RX MEDLINE=92231894; PubMed=1567404;
 RA Tsuzuki K., Kimura K., Fujii N., Yokosawa N., Oguma K.;
 RT "The complete nucleotide sequence of the gene coding for the
 RT nontoxic-nonhemagglutinin component of Clostridium botulinum type C
 RT progenitor toxin."
 RL Biochem. Biophys. Res. Commun. 183:1273-1279(1992).
 CC -!- FUNCTION: THE NONTOXIC COMPONENT IS NECESSARY TO MAINTAIN
 CC TOXICITY.
 CC -----
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 CC -----
 DR EMBL; X62389; CAA44262.1; -.
 DR InterPro; IPR008985; ConA_like_lec_gl.
 DR InterPro; IPR000395; Peptidase_M27.
 DR Pfam; PF01742; Peptidase_M27; 1.
 DR PRINTS; PR00760; BONTXILYSIN.
 DR ProDom; PD001963; Bontoxilysin; 1.
 KW Neurotoxin.
 SQ SEQUENCE 1196 AA; 138740 MW; 4BD5956274D7F9C3 CRC64;

Query Match 45.5%; Score 51; DB 1; Length 1196;
 Best Local Similarity 80.0%; Pred. No. 2.7;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 NNFTVSEFWLR 11
 ||||: ||||
 Db 899 NNFTICEFWLR 908

RESULT 14

BXC1_CLOBO

ID BXC1_CLOBO STANDARD; PRT; 1290 AA.
 AC P18640;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Botulinum neurotoxin type C1 precursor (EC 3.4.24.69) (BoNT/C1)
 DE (Bontoxilysin C1).
 OS Clostridium botulinum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1491;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=90370487; PubMed=2204031;
 RA Hauser D., Eklund M.W., Kurazono H., Binz T., Niemann H., Gill D.M.,
 RA Boquet P., Popoff M.R.;
 RT "Nucleotide sequence of Clostridium botulinum C1 neurotoxin.";
 RL Nucleic Acids Res. 18:4924-4924(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Type C Stockholm / C-ST;
 RX MEDLINE=91024998; PubMed=2222445;
 RA Kimura K., Fujii N., Tsuzuki K., Murakami T., Indoh T.,
 RA Yokosawa N., Takeshi K., Syuto B., Oguma K.;
 RT "The complete nucleotide sequence of the gene coding for botulinum
 RT type C1 toxin in the C-ST phage genome.";
 RL Biochem. Biophys. Res. Commun. 171:1304-1311(1990).
 RN [3]
 RP SEQUENCE OF 2-25.
 RC STRAIN=Type C Stockholm / C-ST;
 RX MEDLINE=88153072; PubMed=2450068;
 RA Tsuzuki K., Yokosawa N., Syuto B., Ohishi I., Fujii N., Kimura K.,
 RA Oguma K.;
 RT "Establishment of a monoclonal antibody recognizing an antigenic site
 RT common to Clostridium botulinum type B, C1, D, and E toxins and
 RT tetanus toxin.";
 RL Infect. Immun. 56:898-902(1988).
 RN [4]
 RP IDENTIFICATION OF SUBSTRATE.
 RX MEDLINE=94038966; PubMed=7901002;
 RA Blasi J., Chapman E.R., Yamasaki S., Binz T., Niemann H., Jahn R.;
 RT "Botulinum neurotoxin C1 blocks neurotransmitter release by means of
 RT cleaving HPC-1/syntaxin.";
 RL EMBO J. 12:4821-4828(1993).
 CC -!- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
 CC RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
 CC AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
 CC WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
 CC INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
 CC ENDOPEPTIDASE THAT CLEAVES SYNTAXIN.
 CC -!- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the
 CC neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No
 CC detected action on small molecule substrates.
 CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -!- SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a
 CC heavy chain (H). The light chain has the pharmacological activity,
 CC while the N- and C-terminal of the heavy chain mediate channel
 CC formation and toxin binding, respectively.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MISCELLANEOUS: There are seven antigenically distinct forms of
 CC botulinum neurotoxin: Types A, B, C1, D, E, F, and G.
 CC -!- MISCELLANEOUS: BOTULINUM TYPE C1 NEUROTOXIN IS SYNTHESIZED BY C
 CC STRAIN OF CLOSTRIDIUM BOTULINUM WHICH CARRY THE APPROPRIATE
 CC BACTERIOPHAGE.
 CC -!- SIMILARITY: Belongs to peptidase family M27.
 CC -----
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CC -----

DR EMBL; X66433; CAA47060.1; -.
DR EMBL; X72793; CAA51313.1; -.
DR EMBL; X53751; CAA37780.1; -.
DR EMBL; D90210; BAA14235.1; -.
DR EMBL; X62389; CAA44263.1; -.
DR HSSP; P10845; 3BTA.
DR MEROPS; M27.002; -.
DR InterPro; IPR008985; ConA_like_lec_gl.
DR InterPro; IPR002160; Kunitz_legume.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR000395; Peptidase_M27.
DR Pfam; PF01742; Peptidase_M27; 1.
DR PRINTS; PR00760; BONTOLILYSIN.
DR ProDom; PD001963; Bontoxilysin; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc.
FT INIT_MET 0 0
FT CHAIN 1 448 BOTULINUM NEUROTOXIN C1, LIGHT-CHAIN.
FT CHAIN 449 1290 BOTULINUM NEUROTOXIN C1, HEAVY-CHAIN.
FT METAL 228 228 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 229 229 BY SIMILARITY.
FT METAL 232 232 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 436 452 INTERCHAIN (PROBABLE).
FT CONFLICT 84 84 P -> T (IN REF. 2).
SQ SEQUENCE 1290 AA; 148734 MW; 71FBE379F97129E8 CRC64;

Query Match 42.9%; Score 48; DB 1; Length 1290;
Best Local Similarity 42.9%; Pred. No. 9;
Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FNNFTVSEFWLRVPK 14
: :|::|||:|: |
Db 934 YESFSISFWIRINK 947

RESULT 15

BXD_CLOBO

ID BXD_CLOBO STANDARD; PRT; 1276 AA.
AC P19321;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Botulinum neurotoxin type D precursor (EC 3.4.24.69) (BoNT/D)
DE (Bontoxilysin D).
GN BOTD.
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BVD/-3;
RX MEDLINE=91016853; PubMed=2216736;

RA Binz T., Kurazono H., Popoff M.R., Eklund M.W., Sakaguchi G.,
 RA Kozaki S., Krieglstein K., Henschen A., Gill D.M., Niemann H.;
 RT "Nucleotide sequence of the gene encoding Clostridium botulinum
 RT neurotoxin type D.";
 RL Nucleic Acids Res. 18:5556-5556(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CB16;
 RX MEDLINE=93042276; PubMed=1420572;
 RA Sunagawa H., Ohyama T., Watanabe T., Inoue K.;
 RT "The complete amino acid sequence of the Clostridium botulinum type D
 RT neurotoxin, deduced by nucleotide sequence analysis of the encoding
 RT phage d-16 phi genome.";
 RL J. Vet. Med. Sci. 54:905-913(1992).
 RN [3]
 RP PARTIAL SEQUENCE.
 RC STRAIN=D-SA, and D-1873;
 RX MEDLINE=89339741; PubMed=2668193;
 RA Moriishi K., Syuto B., Kubo S., Oguma K.;
 RT "Molecular diversity of neurotoxins from Clostridium botulinum type D
 RT strains.";
 RL Infect. Immun. 57:2886-2891(1989).
 RN [4]
 RP IDENTIFICATION OF SUBSTRATE.
 RX MEDLINE=94230352; PubMed=8175689;
 RA Yamasaki S., Baumeister A., Binz T., Blasi J., Link E., Cornille F.,
 RA Roques B., Fykse E.M., Suedhof T.C., Jahn R., Niemann H.;
 RT "Cleavage of members of the synaptobrevin/VAMP family by types D and
 RT F botulinal neurotoxins and tetanus toxin.";
 RL J. Biol. Chem. 269:12764-12772(1994).
 CC -!- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
 CC RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
 CC AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
 CC WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
 CC INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
 CC ENDOPEPTIDASE THAT CLEAVES THE 60-LYS-|-LEU-61 BOND OF
 CC SYNAPTOBREVINS-1 AND -2.
 CC -!- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the
 CC neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No
 CC detected action on small molecule substrates.
 CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -!- SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a
 CC heavy chain (H). The light chain has the pharmacological activity,
 CC while the N- and C-terminal of the heavy chain mediate channel
 CC formation and toxin binding, respectively.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MISCELLANEOUS: There are seven antigenically distinct forms of
 CC botulinum neurotoxin: Types A, B, C1, D, E, F, and G.
 CC -!- MISCELLANEOUS: BOTULINUM TYPE D NEUROTOXIN IS SYNTHESIZED BY D
 CC STRAIN OF CLOSTRIDIUM BOTULINUM WHICH CARRY THE APPROPRIATE
 CC BACTERIOPHAGE.
 CC -!- SIMILARITY: Belongs to peptidase family M27.
 CC -----
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CC -----
DR EMBL; X54254; CAA38175.1; -.
DR EMBL; S49407; AAB24244.1; -.
DR PIR; S11455; S11455.
DR HSSP; P10845; 3BTA.
DR MEROPS; M27.002; -.
DR InterPro; IPR008985; ConA_like_lec_gl.
DR InterPro; IPR002160; Kunitz_legume.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR000395; Peptidase_M27.
DR Pfam; PF01742; Peptidase_M27; 1.
DR PRINTS; PR00760; BONTOXILYSIN.
DR ProDom; PD001963; Bontoxilysin; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc.
FT CHAIN 1 442 BOTULINUM NEUROTOXIN D, LIGHT-CHAIN.
FT CHAIN 443 1276 BOTULINUM NEUROTOXIN D, HEAVY-CHAIN.
FT METAL 229 229 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 230 230 BY SIMILARITY.
FT METAL 233 233 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 437 450 INTERCHAIN (PROBABLE).
FT VARIANT 15 16 ND -> PV (IN STRAIN D-SA).
FT VARIANT 17 18 ND -> LQ (IN STRAIN D-1873).
FT VARIANT 452 452 K -> Q (IN STRAIN D-SA).
FT VARIANT 457 457 R -> T (IN STRAIN D-SA).
FT VARIANT 457 457 R -> F (IN STRAIN D-1873).
FT VARIANT 462 462 A -> D (IN STRAIN D-1873).
FT VARIANT 489 489 K -> N (IN STRAIN CB16).
FT VARIANT 644 644 N -> K (IN STRAIN CB16).
FT VARIANT 1122 1122 Q -> R (IN STRAIN CB16).
SQ SEQUENCE 1276 AA; 146871 MW; C1EC50F46C8233E2 CRC64;

Query Match 42.4%; Score 47.5; DB 1; Length 1276;
Best Local Similarity 40.9%; Pred. No. 11;
Matches 9; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

Qy 1 FNNFTVSEFWLRVPK-VSASHLE 21
: | :|||::: | :: || |
Db 928 YENSSVSFWIKISKDLTNSHNE 949

Search completed: August 13, 2004, 09:13:19
Job time : 1.76923 secs